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QY	241	ATGCGATGCGGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTGCCCACTGAGGAGTCC	300
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QY	301	ACATCACCATGCAGATTATGCGGATCAAACTCCACRAGGCCAGACACATAGGAGAGATG	360
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; Sequence 1, Application US/08718904			
; Patent No. 6037329			
; GENERAL INFORMATION:			
; APPLICANT: Baird, J. Andrew			
; APPLICANT: Chandler, Lois Ann			
; APPLICANT: Sosnowski, Barbara A.			
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGAND			
; NUMBER OF SEQUENCES: 128			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: SEED AND BERRY LLP			
; STREET: 6300 Columbia Center, 701 Fifth Avenue			
; CITY: Seattle			
; STATE: Washington			
; COUNTRY: USA			
; ZIP: 98104-7092			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/718,904			
; FILING DATE: 24-SEP-1996			
; CLASSIFICATION: 424			
; ATTORNEY/AGENT INFORMATION:			
; NAME: No. 6037329tenburg Ph.D., Carol			
; REGISTRATION NUMBER: 39,317			
; REFERENCE/DOCKET NUMBER: 760100.415C1			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (206) 622-4900			
; TELEFAX: (206) 682-6031			
; INFORMATION FOR SEQ ID NO: 1:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 473 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: both			
; MOLECULE TYPE: cDNA			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 13..456			
; OTHER INFORMATION: /product= "VEGF121-encoding DNA"			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: 13..90			
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Db 61 IFQYPPDEIYIFKPSVPLMRCGGCCNDGLEGCVPTESNITMQIMRIKPHOGHIGEM 120  
QY 121 SFLOHNCCECRPKDRARQEK 141  
Db 121 SFLOHNCCECRPKDRARQEK 141  
RESULT 2  
US-09-392-932-1  
; Sequence 1, Application US/09392932  
; Patent No. 6352975  
; GENERAL INFORMATION:  
; APPLICANT: Schreiner, George F.  
; APPLICANT: Johnson, Richard J.  
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND  
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN  
; FILE REFERENCE: SCIOS.002A  
; CURRENT APPLICATION NUMBER: US/09/392,932  
; CURRENT FILING DATE: 1999-09-09  
; EARLIER APPLICATION NUMBER: 60/099,694  
; EARLIER FILING DATE: 1998-09-09  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 147  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
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Best Local Similarity 100.0%; Pred. No. 2.7e-82;  
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QY 121 SFLOHNCCECRPKDRARQEK 141  
Db 121 SFLOHNCCECRPKDRARQEK 141  
RESULT 3  
US-08-706-054A-4  
; Sequence 4, Application US/08706054A  
; Patent No. 6451764  
; GENERAL INFORMATION:  
; APPLICANT: Lee, James  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: VEGF-Related Protein  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/706,054A  
; FILING DATE: 30-Aug-1996  
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/003491  
; FILING DATE: 08-Sep-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: P-40,378  
; REFERENCE/DOCKET NUMBER: P0963R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 147 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
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Db 61 IFQYPPDEIYIFKPSVPLMRCGGCCNDGLEGCVPTESNITMQIMRIKPHOGHIGEM 120  
QY 121 SFLOHNCCECRPKDRARQEK 141  
Db 121 SFLOHNCCECRPKDRARQEK 141  
RESULT 4  
US-08-706-054A-4  
; Patent No. 5240848  
; APPLICANT: KECK, PAMELA J.; CONNOLLY, DANIEL T.; FEDER, JOSEPH  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN VASCULAR  
; PERMEABILITY FACTOR HAVING 189 AMINO ACIDS  
; NUMBER OF SEQUENCES: 11  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/337,037  
; FILING DATE: 10-JUL-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 274,061  
; FILING DATE: 21-NOV-1988  
; SEQ ID NO: 11:  
; LENGTH: 214  
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Query Match 100.0%; Score 792; DB 6; Length 214;  
Best Local Similarity 100.0%; Pred. No. 4.3e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 IFQYPPDEIYIFKPSVPLMRCGGCCNDGLEGCVPTESNITMQIMRIKPHOGHIGEM 120  
QY 121 SFLOHNCCECRPKDRARQEK 141  
Db 121 SFLOHNCCECRPKDRARQEK 141  
RESULT 5  
US-08-807-992B-3  
; Sequence 3, Application US/08807992B





GenCore version 5.1.1.3  
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Title: US-09-884-050-2

Perfect score: 792

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	792	100.0	642	4	US-09-392-932-9
6	792	100.0	648	3	US-08-586-039B-48
7	792	100.0	677	3	US-08-718-904-3
8	792	100.0	677	5	PCT-US95-10973A-27
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12	792	100.0	774	3	US-08-765-340-1

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14	792	100.0	1212	5	PCT-US95-10973A-31	Sequence 31, Appl
15	787	99.4	576	4	US-09-392-932-8	Sequence 8, Appl
16	787	99.4	605	3	US-08-718-904-2	Sequence 2, Appl
17	787	99.4	605	5	PCT-US95-10973A-26	Sequence 26, Appl
18	787	99.4	989	6	5332671-11	Patent No. 5332671
19	787	99.4	990	3	US-08-567-200A-1	Sequence 1, Appl
20	787	99.4	990	3	US-08-691-794-1	Sequence 1, Appl
21	787	99.4	990	4	US-08-882-816-1	Sequence 1, Appl
22	787	99.4	1369	5	PCT-US95-10973A-33	Sequence 33, Appl
23	783	98.9	516	4	US-09-392-932-7	Sequence 7, Appl
24	781.5	98.7	456	5	PCT-US95-10973A-88	Sequence 88, Appl
25	781.5	98.7	467	5	PCT-US95-10973A-86	Sequence 86, Appl
26	776.5	98.0	599	5	PCT-US95-10973A-87	Sequence 87, Appl
27	776.5	98.0	599	5	PCT-US95-10973A-89	Sequence 89, Appl
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29	685.5	86.6	445	3	US-08-586-039B-32	Sequence 32, Appl
30	685.5	86.6	649	3	US-08-586-039B-34	Sequence 34, Appl
31	680.5	85.9	573	3	US-08-586-039B-30	Sequence 30, Appl
32	657	83.0	886	6	5219739-23	Patent No. 5219739
33	656.5	82.9	1167	5	PCT-US95-10973A-57	Sequence 57, Appl
34	656.5	82.9	1557	5	PCT-US95-10973A-78	Sequence 78, Appl
35	651.5	82.3	1299	5	PCT-US95-10973A-58	Sequence 58, Appl
36	649.5	82.0	1809	5	PCT-US95-10973A-79	Sequence 79, Appl
37	640	80.8	498	6	5194596-20	Patent No. 5194596
38	640	80.8	498	6	5219739-21	Patent No. 5219739
39	640	80.8	1269	5	PCT-US95-10973A-32	Sequence 32, Appl
40	570.5	72.0	961	6	5219739-16	Patent No. 5219739
41	562.5	71.0	961	6	5194596-16	Patent No. 5194596
42	525	66.3	789	6	5219739-8	Patent No. 5219739
43	525	66.3	790	6	5194596-8	Patent No. 5194596
44	365	46.2	197	5	PCT-US95-10973A-18	Sequence 18, Appl
45	325	41.0	450	3	US-08-586-039B-46	Sequence 46, Appl

ALIGNMENTS

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Patent No. 6352975  
GENERAL INFORMATION:  
APPLICANT: Schreiner, George F.  
TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND  
FILE REFERENCE: SCIOS.002A  
CURRENT APPLICATION NUMBER: US/09/392,932  
CURRENT FILING DATE: 1999-09-09  
EARLIER APPLICATION NUMBER: 60/099,694  
EARLIER FILING DATE: 1998-09-09  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 444  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-09-392-932-6

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GenCore version 5.1.3  
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2252.488 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	422.8	99.2	648	US-08-586-039B-48	Sequence 48, Appl
3	422.8	99.2	1195	5240848-6	Patent No. 5240848
4	422.4	99.2	444	US-09-392-932-6	Sequence 6, Appli
5	422.4	99.2	473	US-08-718-904-1	Sequence 1, Appli
6	422.4	99.2	473	PCT-US95-10973A-25	Sequence 25, Appl
7	422.4	99.2	774	US-08-765-340-1	Sequence 1, Appli
8	422	99.1	605	US-08-718-904-2	Sequence 2, Appli
9	422	99.1	605	PCT-US95-10973A-26	Sequence 26, Appl
10	421.2	98.9	516	US-09-392-932-7	Sequence 7, Appli
11	421.2	98.9	642	US-09-392-932-9	Sequence 9, Appli
12	421.2	98.9	677	US-08-718-904-3	Sequence 3, Appli
13	421.2	98.9	677	PCT-US95-10973A-27	Sequence 27, Appl
14	421.2	98.9	699	US-09-392-932-10	Sequence 10, Appl
15	421.2	98.9	728	US-08-718-904-4	Sequence 4, Appli
16	421.2	98.9	728	PCT-US95-10973A-28	Sequence 28, Appl
17	420.8	98.8	1212	US-08-718-904-31	Sequence 31, Appl
18	420.4	98.7	576	US-09-392-932-8	Sequence 8, Appli
19	420.4	98.7	989	5332671-11	Patent No. 5332671
20	420.4	98.7	990	US-08-567-200A-1	Sequence 1, Appli
21	420.4	98.7	990	US-08-691-794-1	Sequence 1, Appli
22	420.4	98.7	990	US-08-882-816-1	Sequence 1, Appli
23	420.4	98.7	1369	PCT-US95-10973A-33	Sequence 33, Appl
24	409.4	96.1	456	PCT-US95-10973A-88	Sequence 88, Appl
25	409.4	96.1	467	PCT-US95-10973A-86	Sequence 86, Appl
26	409	96.0	599	PCT-US95-10973A-87	Sequence 87, Appl
27	409	96.0	599	PCT-US95-10973A-89	Sequence 89, Appl

28	366	85.9	1543	6	5332671-5	Patent No. 5332671
29	344.4	80.8	1809	5	PCT-US95-10973A-79	Sequence 79, Appl
30	344	80.8	498	6	5194596-20	Patent No. 5194596
31	342.8	80.5	1167	5	PCT-US95-10973A-57	Sequence 57, Appl
32	342.8	80.5	1557	5	PCT-US95-10973A-78	Sequence 78, Appl
33	342.4	80.4	498	6	5219739-21	Patent No. 5219739
34	342.4	80.4	1299	5	PCT-US95-10973A-32	Sequence 32, Appl
35	342.4	80.4	1299	5	PCT-US95-10973A-58	Sequence 58, Appl
36	325.2	76.3	649	3	US-08-586-039B-34	Sequence 34, Appl
37	324.8	76.2	445	3	US-08-586-039B-32	Sequence 32, Appl
38	324.4	76.2	573	3	US-08-586-039B-30	Sequence 30, Appl
39	293.6	68.9	961	6	5219739-16	Patent No. 5219739
40	290.4	68.2	961	6	5194596-16	Patent No. 5194596
41	271	63.6	789	6	5219739-8	Patent No. 5219739
42	271	63.6	790	6	5194596-8	Patent No. 5194596
43	250	58.7	886	6	5219739-23	Patent No. 5219739
44	197	46.2	197	5	PCT-US95-10973A-18	Sequence 18, Appl
45	134.4	31.5	146	3	US-08-765-340-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1  
US-08-784-551C-1  
; Sequence 1, Application US/08784551C  
; Patent No. 6013780  
; GENERAL INFORMATION:  
; APPLICANT: Gera Neufeld  
; APPLICANT: Eli Keshet  
; APPLICANT: Israel Vlodavsky  
; APPLICANT: Zoya Poltorak  
; TITLE OF INVENTION: ANGIOGENIC FACTOR AND USE THEREOF  
; TITLE OF INVENTION: IN TREATING CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Blank, Rome, Comisky & McCauley LLP  
; STREET: 900 17th Street, N.W.  
; CITY: Suite 1000  
; CITY: Washington, D.C.  
; STATE: N/A  
; COUNTRY: U.S.A.  
; ZIP: 20006  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Fastseq for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/784,551C  
; FILING DATE: January 21, 1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cohen, Herbert  
; REGISTRATION NUMBER: 25,109  
; REFERENCE/DOCKET NUMBER: 0274.005/P003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 463-7700  
; TELEFAX: (202) 463-6915  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 516 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-784-551C-1

Query Match 99.2%; Score 422.8; DB 3; Length 516;



Db 157 ATGAAGTCTTCTGCTGCTTTGGGTGCAATGGAGCCCTTGCTGCTGCTTACCTCCACCAT 216  
Qy 61 GCCAAGTGTGCCAGGCTGCACCCATGGCAGAAAGGAGGCGCAGAAATCATCACCAAGTG 120  
Db 217 GCCAAGTGTGCCAGGCTGCACCCATGGCAGAAAGGAGGCGCAGAAATCATCACCAAGTG 276  
Qy 121 GTGAAGTTCATGGATGCTTATCAGCGCAGCTACTGCCATPCCAATCGAGACCTGTGTGGAC 180  
Db 277 GTGAAGTTCATGGATGCTTATCAGCGCAGCTACTGCCATPCCAATCGAGACCTGTGTGGAC 336  
Qy 181 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTG 240  
Db 337 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTG 396  
Qy 241 ATCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTCGCCACTGAGGATGCC 300  
Db 397 ATCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTCGCCACTGAGGATGCC 456  
Qy 301 AACATCACCATCGAGTATTGGGATCAAACTTCAAGCCACGACATAGGAGAGATG 360  
Db 457 AACATCACCATCGAGTATTGGGATCAAACTTCAAGCCACGACATAGGAGAGATG 516  
Qy 361 AGCTTCTTACAGCAACAATAATGTGAATGCCAGACCAAGAAAGATAGACAGACAAGAA 420  
Db 517 AGCTTCTTACAGCAACAATAATGTGAATGCCAGACCAAGAAAGATAGACAGACAAGAA 576  
Qy 421 AAGTAA 426  
Db 577 AAAAAA 582

RESULT 4  
US-09-392-932-6  
; Sequence 6, Application US/09392932  
; Patent No. 6352975  
; GENERAL INFORMATION:  
; APPLICANT: Schreiner, George F.  
; APPLICANT: Johnson, Richard J.  
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND  
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN  
; FILE REFERENCE: SCIOS.002A  
; CURRENT APPLICATION NUMBER: US/09/392,932  
; CURRENT FILING DATE: 1999-09-09  
; EARLIER APPLICATION NUMBER: 60/099,694  
; EARLIER FILING DATE: 1998-09-09  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 444  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-09-392-932-6

Query Match 99.2%; Score 422.4; DB 4; Length 444;  
Best Local Similarity 99.8%; Pred. No. 7.5e-120;  
Matches 423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAAGTCTTCTGCTGCTTTGGGTGCAATGGAGCCCTTGCTGCTGCTTACCTCCACCAT 60  
Db 1 ATGAAGTCTTCTGCTGCTTTGGGTGCAATGGAGCCCTTGCTGCTGCTTACCTCCACCAT 60  
Qy 61 GCCAAGTGTGCCAGGCTGCACCCATGGCAGAAAGGAGGCGCAGAAATCATCACCAAGTG 120  
Db 61 GCCAAGTGTGCCAGGCTGCACCCATGGCAGAAAGGAGGCGCAGAAATCATCACCAAGTG 120  
Qy 121 GTGAAGTTCATGGATGCTTATCAGCGCAGCTACTGCCATPCCAATCGAGACCTGTGTGGAC 180  
Db 121 GTGAAGTTCATGGATGCTTATCAGCGCAGCTACTGCCATPCCAATCGAGACCTGTGTGGAC 180  
Qy 181 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTG 240  
Db 181 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTG 240

Qy 241 ATCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTCGCCACTGAGGATGCC 300  
Db 241 ATCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTCGCCACTGAGGATGCC 300  
Qy 301 AACATCACCATCGAGATTTATCGGGATCAAACTTCAAGCCACGACATAGGAGAGATG 360  
Db 301 AACATCACCATCGAGATTTATCGGGATCAAACTTCAAGCCACGACATAGGAGAGATG 360  
Qy 361 AGCTTCTTACAGCAACAATAATGTGAATGCCAGACCAAGAAAGATAGACAGACAAGAA 420  
Db 361 AGCTTCTTACAGCAACAATAATGTGAATGCCAGACCAAGAAAGATAGACAGACAAGAA 420  
Qy 421 AAGT 424  
Db 421 AAAT 424

RESULT 5  
US-08-718-904-1  
; Sequence 1, Application US/08718904  
; Patent No. 6037329  
; GENERAL INFORMATION:  
; APPLICANT: Baird, J. Andrew  
; APPLICANT: Chandler, Lois Ann  
; APPLICANT: Sosnowski, Barbara A.  
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERA  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/718,904  
; FILING DATE: 24-SEP-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6037329tenburg Ph.D., Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 760100.415C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 473 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: both  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..456  
; OTHER INFORMATION: /product= "VEGF121-encoding DNA"  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..90  
; OTHER INFORMATION: /product= leader-encoding sequence  
US-08-718-904-1

Query Match 99.2%; Score 422.4; DB 3; Length 473;  
Best Local Similarity 99.8%; Pred. No. 7.7e-120;  
Matches 423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ATGAAGTCTTCTGCTGCTTTGGGTGCAATGGAGCCCTTGCTGCTGCTTACCTCCACCAT 60  
|||||

RESULT 6  
 PCT-US95-10973A-25  
 Sequence 25, Application PC/TUS9510973A  
 GENERAL INFORMATION:  
 APPLICANT: Prism Pharmaceuticals, Inc.  
 TITLE OF INVENTION: CONJUGATES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGET  
 NUMBER OF SEQUENCES: 107  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SEED AND BERRY  
 STREET: 6300 Columbia Center, 701 Fifth Avenue  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 98104-7092  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/10973A  
 FILING DATE: 29-AUG-1995  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nottenburg, Carol  
 REGISTRATION NUMBER: 39,317  
 REFERENCE/DOCKET NUMBER: 760100.413PC  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 TELEFAX: (206) 682-6031  
 INFORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 473 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: both  
 MOLECULE TYPE: CDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 13..456  
 OTHER INFORMATION: /product= "VEGF121-encoding DNA"  
 FEATURE:

RESULT 7  
US-08-765-340-1  
Sequence 1, Application US/08765340  
Patent No. 6150092  
GENERAL INFORMATION:  
APPLICANT: UCHIDA, K.,  
APPLICANT: UCHIDA, T.,  
APPLICANT: TANAKA, Y.,  
APPLICANT: MATSUDA, Y.,  
APPLICANT: KONDO, S.,  
TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID  
NUMBER OF SEQUENCES: 185  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,340  
FILING DATE: 23-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 145146/94



FILING DATE: 27-JUN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 311130/94  
FILING DATE: 21-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: SERUNIAN, LESLIE  
REGISTRATION NUMBER: 35,353  
REFERENCE/DOCKET NUMBER: 1452-4005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 774 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
US-08-765-340-1

Query Match 99.2%; Score 422.4; DB 3; Length 774;  
Best Local Similarity 99.8%; Pred. No. 9.7e-120;  
Matches 423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAATTTCTGCTGCTTTGGTGCAATGGAGCCCTTGCTGCTCTACCTCCACCAT 60  
Db 101 ATGAATTTCTGCTGCTTTGGTGCAATGGAGCCCTTGCTGCTCTACCTCCACCAT 160

Qy 61 GCCAAGTGGTCCAGGCTGCACCCATGCGAAGAGGAGGCGCAGAAATCATCAGAAATG 120  
Db 161 GCCAAGTGGTCCAGGCTGCACCCATGCGAAGAGGAGGCGCAGAAATCATCAGAAATG 220

Qy 121 GTGAAGTTTCATGGATGCTATCAGGCGCAGCTACTGCCATCAATCGAGACCCCTGGTGAC 180  
Db 221 GTGAAGTTTCATGGATGCTATCAGGCGCAGCTACTGCCATCAATCGAGACCCCTGGTGAC 280

Qy 181 ATCTTCCAGGAGTACCCCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 240  
Db 281 ATCTTCCAGGAGTACCCCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 340

Qy 241 ATGGATCGGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCTGCTGCTGCTGCTGCTG 300  
Db 341 ATGGATCGGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCTGCTGCTGCTGCTGCTG 400

Qy 301 AACATCACCATTGCGATTTATGCGGATCAAACTCACCAGGCGCAGCACAATAGGAGAGATG 360  
Db 401 AACATCACCATTGCGATTTATGCGGATCAAACTCACCAGGCGCAGCACAATAGGAGAGATG 460

Qy 361 AGCTTCTTACAGCACAAATGTGAATGCGAGACCAAGAAAGATAGAGCAAGCAAGAA 420  
Db 461 AGCTTCTTACAGCACAAATGTGAATGCGAGACCAAGAAAGATAGAGCAAGCAAGAA 520

Qy 421 AAGT 424  
Db 521 AAAT 524

RESULT 8  
US-08-718-904-2  
Sequence 2, Application US/08718904  
Patent No. 6037329  
GENERAL INFORMATION:  
APPLICANT: Baird, J. Andrew  
APPLICANT: Chandler, Lois Ann  
APPLICANT: Sosnowski, Barbara A.  
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA

ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/718,904  
FILING DATE: 24-SEP-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6037329tenburg Ph.D., Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 760100.415C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 605 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 13..588  
OTHER INFORMATION: /product= "VEGF165-encoding DNA"  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 13..90  
OTHER INFORMATION: /product= "leader sequence-encoding DNA"  
US-08-718-904-2

Query Match 99.1%; Score 422; DB 3; Length 605;  
Best Local Similarity 100.0%; Pred. No. 1.1e-119;  
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAATTTCTGCTGCTTTGGTGCAATGGAGCCCTTGCTGCTCTACCTCCACCAT 60  
Db 13 ATGAATTTCTGCTGCTTTGGTGCAATGGAGCCCTTGCTGCTCTACCTCCACCAT 72

Qy 61 GCCAAGTGGTCCAGGCTGCACCCATGCGAAGAGGAGGCGCAGAAATCATCAGAAATG 120  
Db 73 GCCAAGTGGTCCAGGCTGCACCCATGCGAAGAGGAGGCGCAGAAATCATCAGAAATG 132

Qy 121 GTGAAGTTTCATGGATGCTATCAGGCGCAGCTACTGCCATCAATCGAGACCCCTGGTGAC 180  
Db 133 GTGAAGTTTCATGGATGCTATCAGGCGCAGCTACTGCCATCAATCGAGACCCCTGGTGAC 192

Qy 181 ATCTTCCAGGAGTACCCCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 240  
Db 193 ATCTTCCAGGAGTACCCCTGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 252

Qy 241 ATGGATCGGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCTGCTGCTGCTGCTGCTG 300  
Db 253 ATGGATCGGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCTGCTGCTGCTGCTGCTG 312

Qy 301 AACATCACCATTGCGATTTATGCGGATCAAACTCACCAGGCGCAGCACAATAGGAGAGATG 360  
Db 313 AACATCACCATTGCGATTTATGCGGATCAAACTCACCAGGCGCAGCACAATAGGAGAGATG 372

Qy 361 AGCTTCTTACAGCACAAATGTGAATGCGAGACCAAGAAAGATAGAGCAAGCAAGAA 420  
Db 373 AGCTTCTTACAGCACAAATGTGAATGCGAGACCAAGAAAGATAGAGCAAGCAAGAA 432

Qy 421 AA 422  
Db 433 AA 434

RESULT 9  
PCT-US95-10973A-26

Qy	361	AGCTTCCTACAGCACACAANAATGTGAATCCAGACCACAAAGAAAAGATAGACCAACAAGAA	432
Db	373	AGCTTCCTACAGCACACAANAATGTGAATCCAGACCACAAAGAAAAGATAGACCAACAAGAA	433
Qy	421	AA 422	
Db	433	AA 434	

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RESULT 10
US-09-392-932-7
; Sequence 7, Application US/09392932
; Patent No. 6352975
; GENERAL INFORMATION:
; APPLICANT: Schreiner, George F.
; APPLICANT: Johnson, Richard J.
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN
; FILE REFERENCE: SCIOS.002A
; CURRENT APPLICATION NUMBER: US/09/392,932
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: 60/099,694
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-392-932-7

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Db	121	GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCAATCAGACCCCTGGTGGAC	240
Qy	181	ATCTTCCAGGAGTACCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCCCTG	240
Db	181	ATCTTCCAGGAGTACCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCCCTG	240
Qy	241	ATGCGATGCGGGGCTGCTGCAATGACGAGGGGCTGGAGTGTGTGCCCACTGAGGAGTCC	300
Db	241	ATGCGATGCGGGGCTGCTGCAATGACGAGGGGCTGGAGTGTGTGCCCACTGAGGAGTCC	300
Qy	301	AACATCACCATTGCAGATTATGCGGATCAAACCTCACCAAGGCCAGACACATAGGAGAGATG	360
Db	301	AACATCACCATTGCAGATTATGCGGATCAAACCTCACCAAGGCCAGACACATAGGAGAGATG	360
Qy	361	AGCTTCTTACAGCACACAATGTGAATGCAGACCAACCAAGAAAGATAGACCAACAAGAA	420
Db	361	AGCTTCTTACAGCACACAATGTGAATGCAGACCAACCAAGAAAGATAGACCAACAAGAA	420
Qy	421	AAGTAA 426	
Db	421	AAAAAA 426	

RESULT 11  
 US-09-392-932-9  
 : Sequence 9, Application US/09392932  
 : Patent No. 6352975  
 : GENERAL INFORMATION:

; APPLICANT: Schreiner, George F.  
; APPLICANT: Johnson, Richard J.  
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND  
; FILE REFERENCE: SCIOS.002A  
; CURRENT APPLICATION NUMBER: US/09/392,932  
; CURRENT FILING DATE: 1999-09-09  
; EARLIER APPLICATION NUMBER: 60/099,694  
; EARLIER FILING DATE: 1998-09-09  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 642  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-09-392-932-9

Query Match 98.9%; Score 421.2; DB 4; Length 642;  
Best Local Similarity 99.3%; Pred. No. 2.1e-119;  
Matches 423; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ATGAATTTCTGCTGCTTGGTGCATTGGAGCCTTGCTGCTGCTTACCTCCACCAT 60  
DB 1 ATGAATTTCTGCTGCTTGGTGCATTGGAGCCTTGCTGCTGCTTACCTCCACCAT 60  
QY 61 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAAAGGAGGAGGCAGAAATCATCAGGAAGTG 120  
DB 61 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAAAGGAGGAGGCAGAAATCATCAGGAAGTG 120  
QY 121 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCAAATCGAGACCCTGGTGGAC 180  
DB 121 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCAAATCGAGACCCTGGTGGAC 180  
QY 181 ATCTTCCAGGAGTACCTGATGAGATCGAGTACATCTTCAAGCCCATCTGCTGCCCTG 240  
DB 181 ATCTTCCAGGAGTACCTGATGAGATCGAGTACATCTTCAAGCCCATCTGCTGCCCTG 240  
QY 241 ATGCGATCGGGGGTGTGCTCAATGACGAGGCGCTGGAGTGTGTGCCACTGAGGAGTCC 300  
DB 241 ATGCGATCGGGGGTGTGCTCAATGACGAGGCGCTGGAGTGTGTGCCACTGAGGAGTCC 300  
QY 301 AACATCACCATCGAGATATGCGGATCAAACTCACCAGGCCAGCACATAGAGAGATG 360  
DB 301 AACATCACCATCGAGATATGCGGATCAAACTCACCAGGCCAGCACATAGAGAGATG 360  
QY 361 AGCTTCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAAGATAGAGCAAGAA 420  
DB 361 AGCTTCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAAGATAGAGCAAGAA 420  
QY 421 AAGTAA 426  
DB 421 AAAAAA 426

RESULT 12  
US-08-718-904-3  
; Sequence 3, Application US/08718904  
; Patent No. 6037329  
; GENERAL INFORMATION:  
; APPLICANT: Baird, J. Andrew  
; APPLICANT: Chandler, Lois Ann  
; APPLICANT: Sosnowski, Barbara A.  
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/718,904  
; FILING DATE: 24-SEP-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6037329tenburg Ph.D., Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 760100.415C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 677 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..657  
; OTHER INFORMATION: /product= "VEGF189-encoding DNA"  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..90  
; OTHER INFORMATION: /product= "leader sequence-encoding DNA"  
US-08-718-904-3

Query Match 98.9%; Score 421.2; DB 3; Length 677;  
Best Local Similarity 99.3%; Pred. No. 2.1e-119;  
Matches 423; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ATGAATTTCTGCTGCTTGGTGCATTGGAGCCTTGCTGCTGCTTACCTCCACCAT 60  
DB 13 ATGAATTTCTGCTGCTTGGTGCATTGGAGCCTTGCTGCTGCTTACCTCCACCAT 72  
QY 61 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAAAGGAGGAGGCAGAAATCATCAGGAAGTG 120  
DB 73 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAAAGGAGGAGGCAGAAATCATCAGGAAGTG 132  
QY 121 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCAAATCGAGACCCTGGTGGAC 180  
DB 133 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCAAATCGAGACCCTGGTGGAC 192  
QY 181 ATCTTCCAGGAGTACCTGATGAGATCGAGTACATCTTCAAGCCCATCTGCTGCCCTG 240  
DB 193 ATCTTCCAGGAGTACCTGATGAGATCGAGTACATCTTCAAGCCCATCTGCTGCCCTG 252  
QY 241 ATGCGATCGGGGGTGTGCTCAATGACGAGGCGCTGGAGTGTGTGCCACTGAGGAGTCC 300  
DB 253 ATGCGATCGGGGGTGTGCTCAATGACGAGGCGCTGGAGTGTGTGCCACTGAGGAGTCC 312  
QY 301 AACATCACCATCGAGATATGCGGATCAAACTCACCAGGCCAGCACATAGAGAGATG 360  
DB 313 AACATCACCATCGAGATATGCGGATCAAACTCACCAGGCCAGCACATAGAGAGATG 372  
QY 361 AGCTTCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAAGATAGAGCAAGAA 420  
DB 373 AGCTTCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAAGATAGAGCAAGAA 432  
QY 421 AAGTAA 426  
DB 433 AAAAAA 438  
RESULT 13  
PCT-US95-10973A-27  
; Sequence 27, Application PC/TUS9510973A  
; GENERAL INFORMATION:  
; APPLICANT: Prizm Pharmaceuticals, Inc.



Query Match	98.9%	Score	421.2	DB	3	Length	728
Best Local Similarity	99.3%	Pred. No.	2.2e-119				
Matches	423	Conservative	0	Mismatches	3	Indels	0
QY	1	ATCAACTTTCTGCTGTCCTTGGGTGTCATTGGAGCCTTGCCCTTGCTGCTCTACCTCCACCAT	60				
Db	13	ATGAACTTCTGCTGTCCTTGGGTGTCATTGGAGCCTTGCCCTTGCTGCTCTACCTCCACCAT	72				
QY	61	GCCAAAGTGTCGCCAGGCTGCACCCATGGCAGAAGGAGGGCGCAAGATCATCAAGAAAGTG	120				
Db	73	GCCAAAGTGTCGCCAGGCTGCACCCATGGCAGAAGGAGGGCGCAAGATCATCAAGAAAGTG	132				
QY	121	GTCAAGTTCATGATGCTCTATACGCCAGCTACTGCGCATCCAACTCGAGACCCCTGGTGGAC	180				
Db	133	GTGAAGTTCAATGATGCTCTATACGCCAGCTACTGCGCATCCAACTCGAGACCCCTGGTGGAC	192				
QY	181	ATCTTCCAGAGTAGACCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTGTG	240				
Db	193	ATCTTCCAGAGTAGACCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTGTG	252				
QY	241	ATCGGATCGGGGGCTGCTGCAATGACGAGGGCTGAGTGTGTGCGCCACTGAGGAGTCC	300				
Db	253	ATCGATCGGGGGCTGCTGCAATGACGAGGGCTGAGTGTGTGCGCCACTGAGGAGTCC	312				
QY	301	AACATCACCATTGCAGATTATGCGGATCAAACTCACCAGGCCACGACATAGGAGAGATG	360				
Db	313	AACATCACCATTGCAGATTATGCGGATCAAACTCACCAGGCCACGACATAGGAGAGATG	372				
QY	361	AGTCTCTACAGCACAACTATGTGAATGCAGACCAAGAAAGATAGAGCAAGACAAGAA	420				
Db	373	AGTCTCTACAGCACAACTATGTGAATGCAGACCAAGAAAGATAGAGCAAGACAAGAA	432				

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 20, 2002, 04:57:39 ; Search time 28 Seconds  
(without alignments)  
148.165 Million cell updates/sec

Title: US-09-884-050-2

Perfect score: 792

Sequence: 1 MNFLLSWVHWSLALLYLHH.....FLOHNCCKRPKKDRARQEK 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA.\*

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/PTCUS.COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	792	100.0	147	3	US-08-807-992B-1
2	792	100.0	147	4	US-09-392-932-1
3	792	100.0	147	4	US-08-706-054A-4
4	792	100.0	214	6	5240848-11
5	792	100.0	215	3	US-08-807-992B-3
6	792	100.0	215	4	US-08-586-039B-49
7	792	100.0	215	6	5240848-7
8	792	100.0	232	2	US-08-999-811-7
9	792	100.0	232	2	US-08-824-996-9
10	792	100.0	232	3	US-08-807-992B-4
11	792	100.0	232	3	US-09-042-105-7
12	787	99.4	191	3	US-08-567-200A-2
13	787	99.4	191	3	US-08-807-992B-2
14	787	99.4	191	3	US-08-691-794-2
15	787	99.4	191	4	US-08-795-430-56
16	787	99.4	191	4	US-09-392-932-3
17	787	99.4	191	4	US-09-355-700-56
18	787	99.4	191	4	US-08-882-816-2
19	787	99.4	191	6	5332671-4
20	773.5	97.7	231	5	PCT-US96-09001-10
21	766	96.7	215	6	5219739-22
22	717.5	90.6	190	6	5332671-3
23	685.5	86.6	146	4	US-08-586-039B-33
24	685.5	86.6	214	4	US-08-586-039B-35
25	680.5	85.9	190	4	US-08-586-039B-31
26	672.5	84.9	190	2	US-08-569-063C-20
27	653	82.4	189	1	US-08-469-427A-15

28	645	81.4	121	6	5194596-19	Patent No. 5194596
29	645	81.4	121	6	5219739-20	Patent No. 5219739
30	645	81.4	145	3	US-08-784-551C-2	Sequence 2, Appl
31	645	81.4	145	4	US-09-392-932-2	Sequence 2, Appl
32	640	80.8	165	4	US-08-882-816-3	Sequence 3, Appl
33	640	80.8	165	6	5194596-18	Patent No. 5194596
34	640	80.8	165	6	5219739-19	Patent No. 5219739
35	621	78.4	110	4	US-09-392-932-11	Sequence 11, Appl
36	616	77.8	109	3	US-08-691-794-3	Sequence 3, Appl
37	575.5	72.7	120	6	5194596-9	Patent No. 5194596
38	575.5	72.7	120	6	5219739-9	Patent No. 5219739
39	570.5	72.0	164	6	5194596-17	Patent No. 5194596
40	570.5	72.0	164	6	5219739-17	Patent No. 5219739
41	570.5	72.0	164	6	5219739-18	Patent No. 5219739
42	325	41.0	149	1	US-08-469-427A-14	Sequence 14, Appl
43	325	41.0	149	2	US-08-039-297B-2	Sequence 2, Appl
44	325	41.0	149	2	US-08-569-063C-21	Sequence 21, Appl
45	325	41.0	149	4	US-08-795-430-55	Sequence 55, Appl

## ALIGNMENTS

### RESULT 1

US-08-807-992B-1

; Sequence 1, Application US/08807992B

; Patent No. 6022541

; GENERAL INFORMATION:

; APPLICANT: Senger, Donald R

; APPLICANT: Dvorak, Harold F

; TITLE OF INVENTION: Immunological preparation for concurrent

; TITLE OF INVENTION: specific binding to spatially exposed regions of vascular

; TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blo

; TITLE OF INVENTION: vessel

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David Prashker, Esq.

; STREET: P.O. Box 5387

; CITY: Magnolia

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 01930

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage

; COMPUTER: IBM PS/1

; OPERATING SYSTEM: MS DOS

; SOFTWARE: Wordperfect version 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/807,992B

; FILING DATE: March 3, 1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: David Prashker, Esq.

; REGISTRATION NUMBER: 29,693

; REFERENCE/DOCKET NUMBER: BIS-033

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (978) 525-3794

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 147 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-807-992B-1

Query Match

Best Local Similarity 100.0%; Score 792; DB 3; Length 147;

Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNFLLSWVHWSLALLYLHHAKWSQAAPMAEGGQNNHHEVVKFMDVYORSYCHPIETLVD 60

Db 1 MNFLLSWVHWSLALLYLHHAKWSQAAPMAEGGQNNHHEVVKFMDVYORSYCHPIETLVD 60

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QY 61 IFQEPDEIEYIFKPCVPLMRGCGCCNDGEGLECVPTESNITMQIMRIKPHOGQHIGEM 120
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Db 61 IFQEPDEIEYIFKPCVPLMRGCGCCNDGEGLECVPTESNITMQIMRIKPHOGQHIGEM 120
|||||
QY 121 SFLQHNKCECRPKKDRARQEK 141
|||||
Db 121 SFLQHNKCECRPKKDRARQEK 141
|||||

RESULT 2
US-09-392-932-1
; Sequence 1, Application US/09392932
; Patent No. 6352975
; GENERAL INFORMATION:
; APPLICANT: Schreiner, George F.
; APPLICANT: Johnson, Richard J.
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN
; FILE REFERENCE: SCIOS.002A
; CURRENT APPLICATION NUMBER: US/09/392,932
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: 60/099,694
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-392-932-1

Query Match 100.0%; Score 792; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 2.7e-82;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLLSWVHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETFLVD 60
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Db 1 MNFLLSWVHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETFLVD 60
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QY 61 IFQEPDEIEYIFKPCVPLMRGCGCCNDGEGLECVPTESNITMQIMRIKPHOGQHIGEM 120
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Db 61 IFQEPDEIEYIFKPCVPLMRGCGCCNDGEGLECVPTESNITMQIMRIKPHOGQHIGEM 120
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QY 121 SFLQHNKCECRPKKDRARQEK 141
|||||
Db 121 SFLQHNKCECRPKKDRARQEK 141
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RESULT 3
US-08-706-054A-4
; Sequence 4, Application US/08706054A
; Patent No. 6451764
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: VEGF-Related Protein
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,054A
; FILING DATE: 30-Aug-1996
; CLASSIFICATION: <Unknown>
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/003491
;; FILING DATE: 08-Sep-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER: P-40,378
;; REFERENCE/DOCKET NUMBER: P0963R1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/225-1994
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 147 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-706-034A-4

Query Match 100.0%; Score 792; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 2.7e-82;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNFLLSWVHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETFLVD 60
|||||
QY 61 IFQEPDEIEYIFKPCVPLMRGCGCCNDGEGLECVPTESNITMQIMRIKPHOGQHIGEM 120
|||||
Db 61 IFQEPDEIEYIFKPCVPLMRGCGCCNDGEGLECVPTESNITMQIMRIKPHOGQHIGEM 120
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QY 121 SFLQHNKCECRPKKDRARQEK 141
|||||
Db 121 SFLQHNKCECRPKKDRARQEK 141
|||||

RESULT 4
5240848-11
; Patent No. 5240848
; APPLICANT: KECK, PAMELA J.; CONNOLLY, DANIEL T.; FEDER, JOSEPH
; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN VASCULAR
; PERMEABILITY FACTOR HAVING 189 AMINO ACIDS
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/337,037
; FILING DATE: 10-JUL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 274,061
; FILING DATE: 21-NOV-1988
; SEQ ID NO:11:
; LENGTH: 214
5240848-11

Query Match 100.0%; Score 792; DB 6; Length 214;
Best Local Similarity 100.0%; Pred. No. 4.3e-82;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 IFQEPDEIEYIFKPCVPLMRGCGCCNDGEGLECVPTESNITMQIMRIKPHOGQHIGEM 120
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QY 121 SFLQHNKCECRPKKDRARQEK 141
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Db 121 SFLQHNKCECRPKKDRARQEK 141
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RESULT 5
US-08-807-992B-3
; Sequence 3, Application US/08807992B
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; Patent No. 6022541  
; GENERAL INFORMATION:  
; APPLICANT: Senger, Donald R  
; APPLICANT: Dvorak, Harold F  
; TITLE OF INVENTION: Immunological preparation for concurrent  
; TITLE OF INVENTION: specific binding to spatially exposed regions of vascular  
; TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blood  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David Prashker, Esq.  
; STREET: P.O. Box 5387  
; CITY: Magnolia  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 01930  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
; COMPUTER: IBM PS/1  
; OPERATING SYSTEM: MS DOS  
; SOFTWARE: WordPerfect version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/807,992B  
; FILING DATE: March 3, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David Prashker, Esq.  
; REGISTRATION NUMBER: 29,693  
; REFERENCE/DOCKET NUMBER: BIS-033  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (978) 525-3794  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 215 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-807-992B-3  
Query Match 100.0%; Score 792; DB 3; Length 215;  
Best Local Similarity 100.0%; Pred. No. 4.3e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
Qy 121 SFLQHNKCECRPKKDRARQEK 141  
Db 121 SFLQHNKCECRPKKDRARQEK 141  
RESULT 6  
US-08-586-039B-49  
; Sequence 49, Application US/08586039B  
; Patent No. 6140073  
; GENERAL INFORMATION:  
; APPLICANT: Bayne, Marvin L.  
; APPLICANT: Thomas Jr., Kenneth A.  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C  
; TITLE OF INVENTION: SUBUNIT  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: 126 E. Lincoln Avenue  
; CITY: Rahway  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07065-0900

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Microsoft Word 6  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/586,039B  
; FILING DATE: 16-JAN-1996  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/124,259  
; FILING DATE: 20-SEP-1993  
; APPLICATION NUMBER: 07/676,436  
; FILING DATE: 28-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hand, J. Mark  
; REGISTRATION NUMBER: 36,545  
; REFERENCE/DOCKET NUMBER: 18361DA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-3905  
; TELEFAX: (908) 594-4720  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 215 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-586-039B-49  
Query Match 100.0%; Score 792; DB 4; Length 215;  
Best Local Similarity 100.0%; Pred. No. 4.3e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNFLLSWVHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
Db 1 MNFLLSWVHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
Qy 121 SFLQHNKCECRPKKDRARQEK 141  
Db 121 SFLQHNKCECRPKKDRARQEK 141  
RESULT 7  
5240848-7  
; Patent No. 5240848  
; APPLICANT: KECK, PAMELA J.; CONNOLLY, DANIEL T.; FEDER, JOSEPH  
; TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN VASCULAR  
; PERMEABILITY FACTOR HAVING 189 AMINO ACIDS  
; NUMBER OF SEQUENCES: 11  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/337,037  
; FILING DATE: 10-JUL-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 274,061  
; FILING DATE: 21-NOV-1988  
; SEQ ID NO: 7:  
; LENGTH: 215  
5240848-7  
Query Match 100.0%; Score 792; DB 6; Length 215;  
Best Local Similarity 100.0%; Pred. No. 4.3e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MNFLLSWVHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
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Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
Qy 121 SFLQHNKCECRPKKDRARQEK 141  
Db 121 SFLQHNKCECRPKKDRARQEK 141

Db 61 IFOEYPDEIEYIFKPCVPLMRGCGCCNDGLELCVPTESNITMQIMRIKPHOGQHIGEM 120

QY 121 SFLQHNKCECRPKKDRARQEK 141  
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Db 121 SFLQHNKCECRPKKDRARQEK 141

RESULT 8

US-08-999-811-7

; Sequence 7, Application US/08999811

; Patent No. 5932540

; GENERAL INFORMATION:

; APPLICANT: HU, JING-SHAN

; APPLICANT: ROSEN, CRAIG A.

; APPLICANT: CAO, LIANG

; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX

; STREET: 1100 NEW YORK AVENUE

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/999,811

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/207,550

; FILING DATE: 8-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/465,968

; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: MARKOWICZ, KAREN R.

; REGISTRATION NUMBER: 36,351

; REFERENCE/DOCKET NUMBER: 1488.1000004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)371-2600

; TELEFAX: (202)371-2540

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 232 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: not relevant

; MOLECULE TYPE: protein

US-08-999-811-7

Query Match 100.0%; Score 792; DB 2; Length 232;  
Best Local Similarity 100.0%; Pred. No. 4.8e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNFLSWVHWSLALLYLHHAKWSQAAPMAEGGQNHHEVYVKFMDVYQRSYCHPIETLVD 60  
|||||

QY 61 IFOEYPDEIEYIFKPCVPLMRGCGCCNDGLELCVPTESNITMQIMRIKPHOGQHIGEM 120  
|||||

Db 61 IFOEYPDEIEYIFKPCVPLMRGCGCCNDGLELCVPTESNITMQIMRIKPHOGQHIGEM 120  
|||||

QY 121 SFLQHNKCECRPKKDRARQEK 141  
|||||

Db 121 SFLQHNKCECRPKKDRARQEK 141

RESULT 9

US-08-824-996-9

; Sequence 9, Application US/08824996B

; Patent No. 5935820

; GENERAL INFORMATION:

; APPLICANT: HU, JING-SHAN

; APPLICANT: ROSEN, CRAIG A.

; APPLICANT: CAO, LIANG

; TITLE OF INVENTION: Polynucleotides Encoding Vascular Endothelial Growth

; FILE REFERENCE: PF112DI

; CURRENT APPLICATION NUMBER: US/08/824,996B

; CURRENT FILING DATE: 1997-03-27

; EARLIER APPLICATION NUMBER: 08/207,550

; EARLIER FILING DATE: 1994-03-08

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 9

; LENGTH: 232

; TYPE: PRT

; ORGANISM: Homo sapiens

US-08-824-996-9

Query Match 100.0%; Score 792; DB 2; Length 232;  
Best Local Similarity 100.0%; Pred. No. 4.8e-82;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLSWVHWSLALLYLHHAKWSQAAPMAEGGQNHHEVYVKFMDVYQRSYCHPIETLVD 60  
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Db 1 MNFLSWVHWSLALLYLHHAKWSQAAPMAEGGQNHHEVYVKFMDVYQRSYCHPIETLVD 60  
|||||

QY 61 IFOEYPDEIEYIFKPCVPLMRGCGCCNDGLELCVPTESNITMQIMRIKPHOGQHIGEM 120  
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Db 61 IFOEYPDEIEYIFKPCVPLMRGCGCCNDGLELCVPTESNITMQIMRIKPHOGQHIGEM 120  
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QY 121 SFLQHNKCECRPKKDRARQEK 141  
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Db 121 SFLQHNKCECRPKKDRARQEK 141

RESULT 10

US-08-807-992B-4

; Sequence 4, Application US/08807992B

; Patent No. 6022541

; GENERAL INFORMATION:

; APPLICANT: Senger, Donald R

; APPLICANT: Dvorak, Harold F

; TITLE OF INVENTION: Immunological preparation for concurrent

; TITLE OF INVENTION: specific binding to spatially exposed regions of vascular

; TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated bio

; TITLE OF INVENTION: vessel

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David Prashker, Esq.

; STREET: P.O. Box 5387

; CITY: Magnolia

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 01930

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage

; COMPUTER: IBM PS/1

; OPERATING SYSTEM: MS DOS

; SOFTWARE: WordPerfect version 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/807,992B

; FILING DATE: March 3, 1997

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: David Prashker, Esq.

; REGISTRATION NUMBER: 29,693

; REFERENCE/DOCKET NUMBER: BIS-033

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (978) 525-3794

```
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-807-992B-4

Query Match      100.0%; Score 792; DB 3; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.8e-82;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 IFOEYPDEIEYFKPSCVPLMRCGGCCNDGEGLECYPTESNITMQIMRKPHQGOHIGEM 120
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DB 61 IFOEYPDEIEYFKPSCVPLMRCGGCCNDGEGLECYPTESNITMQIMRKPHQGOHIGEM 120
    |||||||
QY 121 SFLQHNKCECRPKDRARQEK 141
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DB 121 SFLQHNKCECRPKDRARQEK 141
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RESULT 11
US-09-042-105-7
; Sequence 7, Application US/09042105
; Patent No. 6040157
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042.105
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,550
; FILING DATE: 8-MAR-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TO BE ASSIGNED
; FILING DATE: 24-DEC-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ERIC K. STEFFE
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1000003/EKS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-09-042-105-7

Query Match      100.0%; Score 792; DB 3; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.8e-82;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLLSWVHSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRSYCHPIETLVD 60
    |||||||
DB 1 MNFLLSWVHSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRSYCHPIETLVD 60
    |||||||
QY 61 IFOEYPDEIEYFKPSCVPLMRCGGCCNDGEGLECYPTESNITMQIMRKPHQGOHIGEM 120
    |||||||
DB 61 IFOEYPDEIEYFKPSCVPLMRCGGCCNDGEGLECYPTESNITMQIMRKPHQGOHIGEM 120
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QY 121 SFLQHNKCECRPKDRARQEK 141
    |||||||
DB 121 SFLQHNKCECRPKDRARQEK 141
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RESULT 12
US-08-567-200A-2
; Sequence 2, Application US/08567200A
; Patent No. 6020473
; GENERAL INFORMATION:
; APPLICANT: Keyt, Bruce A.
; APPLICANT: Nguyen, Francis H.
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Variants of Vascular Endothelial Cell
; TITLE OF INVENTION: Growth Factor, Their Uses, and Processes for their
; TITLE OF INVENTION: Production
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/567,200A
; FILING DATE: 05-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: dregger, walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-62326-1/WHd
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-567-200A-2

Query Match      99.4%; Score 787; DB 3; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.4e-81;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLLSWVHSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRSYCHPIETLVD 60
    |||||||
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Db 1 MNFLSWVHWSLALLYLHHAQWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
QY 61 IFQEPDELEYIFKPSVPLMRGCGCCNDEGLECVPTESNITQIMRIKPHQGHIGEM 120  
Db 61 IFQEPDELEYIFKPSVPLMRGCGCCNDEGLECVPTESNITQIMRIKPHQGHIGEM 120  
QY 121 SFLQHNKCECRPKKDRARQE 140  
Db 121 SFLQHNKCECRPKKDRARQE 140

## RESULT 13

US-08-807-992B-2  
; Sequence 2, Application US/08807992B  
; Patent No. 6022541  
; GENERAL INFORMATION:  
; APPLICANT: Senger, Donald R  
; APPLICANT: Dvorak, Harold F  
; TITLE OF INVENTION: Immunological preparation for concurrent  
; TITLE OF INVENTION: specific binding to spatially exposed regions of vascular  
; TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blood  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David Prashker, Esq.  
; STREET: P.O. Box 5387  
; CITY: Magnolia  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 01930  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage  
; COMPUTER: IBM PS/1  
; OPERATING SYSTEM: MS DOS  
; SOFTWARE: WordPerfect version 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/807,992B  
; FILING DATE: March 3, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David Prashker, Esq.  
; REGISTRATION NUMBER: 29,693  
; REFERENCE/DOCKET NUMBER: BIS-033  
; TELEPHONE: (978) 525-3794  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 191 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-807-992B-2

Query Match 99.4%; Score 787; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.4e-81;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLSWVHWSLALLYLHHAQWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
Db 1 MNFLSWVHWSLALLYLHHAQWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
QY 61 IFQEPDELEYIFKPSVPLMRGCGCCNDEGLECVPTESNITQIMRIKPHQGHIGEM 120  
Db 61 IFQEPDELEYIFKPSVPLMRGCGCCNDEGLECVPTESNITQIMRIKPHQGHIGEM 120  
QY 121 SFLQHNKCECRPKKDRARQE 140  
Db 121 SFLQHNKCECRPKKDRARQE 140

## RESULT 14

US-08-691-794-2  
; Sequence 2, Application US/08691794

; Patent No. 6057428  
; GENERAL INFORMATION:  
; APPLICANT: Keyt, Bruce A.  
; APPLICANT: Nguyen, Francis H.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Cunningham, Brian C.  
; APPLICANT: Wells, James A.  
; APPLICANT: Li, Bing  
; TITLE OF INVENTION: Variants of Vascular Endothelial Cell  
; TITLE OF INVENTION: Growth Factor, Their Uses, and Processes for their  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/691,794  
; FILING DATE: 02-AUG-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/002,827  
; FILING DATE: 25-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/567,200  
; FILING DATE: 05-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-63758/WHO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELETYPE: 910 277299  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 191 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-691-794-2

Query Match 99.4%; Score 787; DB 3; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.4e-81;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLSWVHWSLALLYLHHAQWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
Db 1 MNFLSWVHWSLALLYLHHAQWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
QY 61 IFQEPDELEYIFKPSVPLMRGCGCCNDEGLECVPTESNITQIMRIKPHQGHIGEM 120  
Db 61 IFQEPDELEYIFKPSVPLMRGCGCCNDEGLECVPTESNITQIMRIKPHQGHIGEM 120  
QY 121 SFLQHNKCECRPKKDRARQE 140  
Db 121 SFLQHNKCECRPKKDRARQE 140

## RESULT 15

US-08-795-430-56  
; Sequence 56, Application US/08795430  
; Patent No. 6130071  
; GENERAL INFORMATION:  
; APPLICANT: Allcalo, Karl

Job time : 30 secs

APPLICANT: Joukov, Vladimir  
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)  
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/795,430  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FI96/00427  
FILING DATE: 01-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/671,573  
FILING DATE: 28-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/601,132  
FILING DATE: 14-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585,895  
FILING DATE: 12-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/510,133  
FILING DATE: 01-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/340,011  
FILING DATE: 14-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28967/33691  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 191 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-430-56

Query Match 99.4%; Score 787; DB 4; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.4e-81;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MNFLLSWYHSLALLYLHAKWSQAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD	60
Qy	61	IFQEYPDEIEYIFKPCVPLMRCGCCNDGEGLECVPTESNITMQIMRIKPHQGQIHGM	120
Db	61	IFQEYPDEIEYIFKPCVPLMRCGCCNDGEGLECVPTESNITMQIMRIKPHQGQIHGM	120
Qy	121	SFLQHNKCECRPKDRARQE	140
Db	121	SFLQHNKCECRPKDRARQE	140

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 20, 2002, 05:02:33 ; Search time 56 Seconds

(without alignments)  
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Title: US-09-884-050-2

Perfect score: 792

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Total number of hits satisfying chosen parameters: 882724

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Issued Patents\_NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	792	100.0	444	4	US-09-392-932-6	Sequence 6, Appli
2	792	100.0	473	4	US-08-718-904-1	Sequence 1, Appli
3	792	100.0	473	5	PCT-US95-10973A-25	Sequence 25, Appl
4	792	100.0	516	3	US-08-784-551C-1	Sequence 1, Appli
5	792	100.0	642	4	US-09-392-932-9	Sequence 9, Appli
6	792	100.0	648	3	US-08-586-039B-48	Sequence 48, Appli
7	792	100.0	677	3	US-08-718-904-3	Sequence 3, Appli
8	792	100.0	677	5	PCT-US95-10973A-27	Sequence -27, Appl
9	792	100.0	699	4	US-09-392-932-10	Sequence 10, Appl
10	792	100.0	728	3	US-08-718-904-4	Sequence 4, Appli
11	792	100.0	728	5	PCT-US95-10973A-28	Sequence 28, Appl
12	792	100.0	774	3	US-08-765-340-1	Sequence 1, Appli

13	792	100.0	1195	6	5240848-6	Patent No. 5240848
14	792	100.0	1212	5	PCT-US95-10973A-31	Sequence 31, Appl
15	787	99.4	576	4	US-09-392-932-8	Sequence 8, Appli
16	787	99.4	605	3	US-08-718-904-2	Sequence 2, Appli
17	787	99.4	605	5	PCT-US95-10973A-26	Sequence 26, Appl
18	787	99.4	989	6	5332671-11	Patent No. 5332671
19	787	99.4	990	3	US-08-567-200A-1	Sequence 1, Appli
20	787	99.4	990	3	US-08-691-794-1	Sequence 1, Appli
21	787	99.4	990	4	US-08-882-816-1	Sequence 1, Appli
22	787	99.4	1369	5	PCT-US95-10973A-33	Sequence 33, Appli
23	783	98.9	516	4	US-09-392-932-7	Sequence 7, Appli
24	781.5	98.7	456	5	PCT-US95-10973A-88	Sequence 88, Appl
25	781.5	98.7	467	5	PCT-US95-10973A-86	Sequence 86, Appl
26	776.5	98.0	599	5	PCT-US95-10973A-87	Sequence 87, Appl
27	776.5	98.0	599	5	PCT-US95-10973A-89	Sequence 89, Appl
28	717.5	90.6	1543	6	5332671-5	Patent No. 5332671
29	685.5	86.6	445	3	US-08-586-039B-32	Sequence 32, Appl
30	685.5	86.6	649	3	US-08-586-039B-34	Sequence 34, Appl
31	680.5	85.9	573	3	US-08-586-039B-30	Sequence 30, Appl
32	657	83.0	886	6	5219739-23	Patent No. 5219739
33	656.5	82.9	1167	5	PCT-US95-10973A-57	Sequence 57, Appl
34	656.5	82.9	1557	5	PCT-US95-10973A-78	Sequence 78, Appl
35	651.5	82.3	1299	5	PCT-US95-10973A-58	Sequence 58, Appl
36	649.5	82.0	1809	5	PCT-US95-10973A-79	Sequence 79, Appl
37	640	80.8	498	6	5194596-20	Patent No. 5194596
38	640	80.8	498	6	5219739-21	Patent No. 5219739
39	640	80.8	1269	5	PCT-US95-10973A-32	Sequence 32, Appl
40	570.5	72.0	961	6	5219739-16	Patent No. 5219739
41	562.5	71.0	961	6	5194596-16	Patent No. 5194596
42	525	66.3	789	6	5219739-8	Patent No. 5219739
43	525	66.3	790	6	5194596-8	Patent No. 5194596
44	366	46.2	197	5	PCT-US95-10973A-18	Sequence 18, Appl
45	325	41.0	450	3	US-08-586-039B-46	Sequence 46, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-392-932-6  
; Sequence 6, Application US/09392932  
; Patent No. 6352975  
; GENERAL INFORMATION:  
; APPLICANT: Schreiner, George F.  
; APPLICANT: Johnson, Richard J.  
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND  
; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN  
; FILE REFERENCE: SCIOS.002A  
; CURRENT APPLICATION NUMBER: US/09/392,932  
; CURRENT FILING DATE: 1999-09-09  
; EARLIER APPLICATION NUMBER: 60/099,694  
; EARLIER FILING DATE: 1998-09-09  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 444  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-09-392-932-6

Alignment Scores:	Pred. No.:	Score:	5:38e-93	Length:	444
Percent Similarity:	792.00	100.00%	Matches:	141	
Best Local Similarity:	100.00%	Conservative:	0		
Query Match:	100.00%	Mismatches:	0		
DB:	4	Indels:	0		
		Gaps:	0		

US-09-884-050-2 (1-141) x US-09-392-932-6 (1-444)

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DB 1 ATGAACCTTCTGCTGCTTGGTGCATTGGAGCCCTGCTGCTTACCTCCACCAT 60





REFERENCE/DOCKET NUMBER: 760100.413PC  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 473 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 13..456  
OTHER INFORMATION: /product= "VEGF121-encoding DNA"  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 13..90  
OTHER INFORMATION: /product= leader-encoding sequence  
PCT-US95-10973A-25

Alignment Scores:  
Pred. No.: 5,89e-93 Length: 473  
Score: 792.00 Matches: 141  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-09-884-050-2 (1-141) x PCT-US95-10973A-25 (1-473)

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Qy 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlyGlnAsnHisGluVal 40  
Db 73 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 132  
Qy 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
Db 133 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCTGGTGAC 192  
Qy 61 IlePheGlnGluTyrProAspGluLeuGluTyrIlePheLysProSerCysValProLeu 80  
Db 193 ATCTTCCAGGAGTACCTGATCAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTG 252  
Qy 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
Db 253 ATGCGATGCGGGGCTGCTGCAATGCGAGGCGCTGGAGTGTGTGCCACTGAGGAGTCC 312  
Qy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisGluMet 120  
Db 313 ACATCACCATCCAGATATGCGGATCAACCTCACCAGGCGCAGACATAGGAGAGATG 372  
Qy 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
Db 373 AGCTTCTTACACGACACAAATGTGAATGCAGACCAAGAAAGATAGACAGACAAAGAA 432  
Qy 141 Lys 141  
Db 433 AAA 435

## RESULT 4

US-08-784-551C-1

Sequence 1, Application US/08784551C  
Patent No. 6013780

GENERAL INFORMATION:

APPLICANT: Gera Neufeld

APPLICANT: Eli Keshet

APPLICANT: Israel Vlodavsky

APPLICANT: Zoya Poltorak

TITLE OF INVENTION: ANGIOGENIC FACTOR AND USE THEREOF

TITLE OF INVENTION: IN TREATING CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Blank, Rome, Comisky & McCauley LLP  
STREET: 900 17th Street, N.W.  
STREET: Suite 1000  
CITY: Washington, D.C.  
STATE: N/A  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/784,551C  
FILING DATE: January 21, 1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Herbert  
REGISTRATION NUMBER: 25,109  
REFERENCE/DOCKET NUMBER: 0274.005/P003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 463-7700  
TELEFAX: (202) 463-6915  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 516 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-784-551C-1  
Alignment Scores:  
Pred. No.: 6,67e-93 Length: 516  
Score: 792.00 Matches: 141  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

US-09-884-050-2 (1-141) x US-08-784-551C-1 (1-516)

Qy 1 MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuLeuTyrLeuHisHis 20  
Db 1 ATGAACCTTCTGCTGCTTGGTGCGATTGGAGCCCTTGCCTGCTGCTACCTCCACCAT 60  
Qy 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlyGlnAsnHisGluVal 40  
Db 61 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
Qy 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
Db 121 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCTGGTGAC 180  
Qy 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
Db 181 ATCTTCCAGGAGTACCTGATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCCTG 240  
Qy 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
Db 241 ATGCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCCACTGAGGAGTCC 300  
Qy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisGluMet 120  
Db 301 AACATCACCATGCAGATTATGCGGATCAAACTCACCAGGCGCAGACATAGGAGATG 360

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QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140
DB 361 AGCTTCTACGACACAAATGTGAATGAGTGCAGACCAAGAAAGATAGACGACAAAGAA 420
QY 141 Lys 141
DB 421 AAA 423
RESULT 5
US-09-392-932-9
; Sequence 9, Application US/09392932
; Patent No. 6352975
; GENERAL INFORMATION:
; APPLICANT: Schreiner, George F.
; APPLICANT: Johnson, Richard J.
; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND
; FILE REFERENCE: SCIOS.002A
; CURRENT APPLICATION NUMBER: US/09/392,932
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: 60/099,694
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-392-932-9
Alignment Scores:
Pred. No.: 9,12e-93 Length: 642
Score: 792.00 Matches: 141
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-884-050-2 (1-141) x US-09-392-932-9 (1-642)
QY 1 MetAsnPheLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20
DB 1 ATGAATTTCTGCTGCTGTTGGTGCAITGGAGCCTCGCCTTGCTGCTCTACCTCCACCAT 60
QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluVal 40
DB 61 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60
DB 121 GTCAAGTTCATGGATGCTATACGCGCAGCTACTGCCATCCATCGAGACCCTGGTGGAC 180
QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80
DB 181 ATCTTCAGAGGTACCTCATGATGATCGATGATCATCTTCAAGCCATCCGTGTGCCCCCTG 240
QY 81 MetArgCysGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100
DB 241 ATCGGATGCGGGGCTGCTGCAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTCC 300
QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120
DB 301 AACATCACCATGCGAGATTATGCGGATCAACACCTTCACCAAGGCCAGCACATAGAGAGATG 360
QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140
DB 361 AGCTTCTACGACACAAATGTGAATGAGTGCAGACCAAGAAAGATAGACGACAAAGAA 420
QY 141 Lys 141
DB 421 AAA 423
RESULT 6
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US-08-586-039B-48
; Sequence 48, Application US/08586039B
; Patent No. 6140073
; GENERAL INFORMATION:
; APPLICANT: Bayne, Marvin L.
; APPLICANT: Thomas Jr., Kenneth A.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR C
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,039B
; FILING DATE: 16-JAN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/124,259
; FILING DATE: 20-SEP-1993
; APPLICATION NUMBER: 07/676,436
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hand, J. Mark
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18361DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 648 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..648
US-08-586-039B-48
Alignment Scores:
Pred. No.: 9,24e-93 Length: 648
Score: 792.00 Matches: 141
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-884-050-2 (1-141) x US-08-586-039B-48 (1-648)
QY 1 MetAsnPheLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20
DB 1 ATGAATTTCTGCTGCTGTTGGTGCAITGGAGCCTTGCTGCTCTACCTCCACCAT 60
QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluVal 40
DB 61 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 120
QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60
DB 121 GTGAAGTTCATGGATGCTATACGCGCAGCTACTGCCATCCATCGAGACCCTGGTGGAC 180
QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80
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Db 181 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTG 240  
Qy 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
Db 241 ATGCGATCGGGGGCTGCTGCAATACGAGGCGCTGGAGTGTGTCGCCACTGAGAGTCC 300  
Qy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
Db 301 AACATCACCATGCAGATTATGGGATCAACCTCACCAGGCCAGCACATAGGAGATG 360  
Qy 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
Db 361 AGCTTCTTACAGCACACAATGTGAATGCAGACCAAGAAAGATAGAGCAAGAA 420  
Qy 141 Lys 141  
Db 421 AAA 423

RESULT 7  
US-08-718-904-3  
; Sequence 3, Application US/08718904  
; Patent No. 6037329  
; GENERAL INFORMATION:  
; APPLICANT: Baird, J. Andrew  
; APPLICANT: Chandler, Lois Ann  
; APPLICANT: Sosnowski, Barbara A.  
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/718,904  
; FILING DATE: 24-SEP-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6037329tenburg Ph.D., Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 760100.415C1  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 677 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..657  
; OTHER INFORMATION: /product= "VEGF189-encoding DNA"  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..90  
; OTHER INFORMATION: /product= "leader sequence-encoding DNA"

US-08-718-904-3  
Alignment Scores:  
Pred. No.: 9,83e-93 Length: 677  
Score: 792.00 Matches: 141  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
US-09-884-050-2 (1-141) x US-08-718-904-3 (1-677)  
Qy 1 MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20  
Db 13 ATGAACCTTCTGCTGCTTGGTGCATTGGAGCCTTGCTTGTCTGTCTACCTCCACCAT 72  
Qy 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40  
Db 73 GCCAAGTGGTCCAGCTGCACCCATGCGAAGAGGAGGCGAGAATCATCAGCAAGTG 132  
Qy 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
Db 133 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCATCGAGACCCTGTGGAC 192  
Qy 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
Db 193 ATCTTCCAGGAGTACCCCTGATGATCGATCGATACATCTTCAAGCCATCCTGTGCCCCGTG 252  
Qy 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
Db 253 ATCGATCGGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCTCCACTGAGGAGTCC 312  
Qy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
Db 313 AACATCACCATGCAGATTATGGGATCAACCTCACCAGGCCAGCACATAGGAGATG 372  
Qy 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
Db 373 AGCTTCTTACAGCACACAATGTGAATGCAGACCAAGAAAGATAGAGCAAGAA 432  
Qy 141 Lys 141  
Db 433 AAA 435

RESULT 8  
PCT-US95-10973A-27  
; Sequence 27, Application PC/TUS9510973A  
; GENERAL INFORMATION:  
; APPLICANT: Prizm Pharmaceuticals, Inc.  
; TITLE OF INVENTION: CONJUGATES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGE  
; NUMBER OF SEQUENCES: 107  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/10973A  
; FILING DATE: 29-AUG-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Nottenburg, Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 760100.413PC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 677 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: both



81 MetaTgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
253 ATGCGATCGGGGGTGCTGCAATACGAGGGCTGGAGTGTGTGCCACTGAGGATCC 312  
101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
313 AACATCACCATGCAGATTATCGGGATCAACCTCACCAGGCCAGCACATAGGAGAGATG 372  
121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140



Qy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyMet 120  
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 Db 457 AACATCACCATGCAGATTATCGGATCAAACTCAACCAAGCCAGCACATAGGAGATG 516  
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 Qy 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
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 Db 517 AGCTTCCTACAGCACAAACAAATGTAATGCAGACCAAGAAAGATAGAGCAAGCAAGAA 576  
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 Qy 141 Lys 141  
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 Db 577 AAA 579

## RESULT 14

PCT-US95-10973A-31  
 ; Sequence 31, Application PC/TUS9510973A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Prizm Pharmaceuticals, Inc.  
 ; TITLE OF INVENTION: CONJUGATES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGET  
 ; NUMBER OF SEQUENCES: 107  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SEED and BERRY  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: USA  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/10973A  
 ; FILING DATE: 29-AUG-1995  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Nottenburg, Carol  
 ; REGISTRATION NUMBER: 39,317  
 ; REFERENCE/DOCKET NUMBER: 760100.413PC  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 31:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1212 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: both  
 ; TOPOLOGY: both  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 4..1212  
 ; OTHER INFORMATION: /product= "VEGF121-SAP LEADER"  
 ; OTHER INFORMATION: p21B"  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 4..81  
 ; OTHER INFORMATION: /product= "LEADER"  
 PCT-US95-10973A-31

Alignment Scores:  
 Pred. No.: 2.26e-92 Length: 1212  
 Score: 792.00 Matches: 141  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 5 Gaps: 0

US-09-884-050-2 (1-141) x PCT-US95-10973A-31 (1-1212)

Qy 1 MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20  
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 Db 4 ATGAACCTTCTGCTCTTGGTGATGGAGCCCTTGCTTGTCTGTCTACCTCCACCAT 63

Qy 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluVal 40  
 |||||  
 Db 64 GCCAAGTGTCCAGGCTGCACCAATGCGCAGAGGAGGAGGAGCAATCATCACGAAGTG 123  
 |||||  
 Qy 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
 |||||  
 Db 124 GTGAAGTTTCATGGATGTCTATCAGCGCAGCTACTGCCATCCAATCGAGACCCCTGGTGAC 183  
 |||||  
 Qy 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
 |||||  
 Db 184 ATCTTCCAGGAGTAGCCCTGATGAGATCGAGTACATCTTCAAGCCCATCTGTGTGCCCTG 243  
 |||||  
 Qy 81 MetArgCysGlyGlyCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
 |||||  
 Db 244 ATGCGATCGGGGGCTGCTCAATGACGAGGCGCTGGAGTGTGTCCCACTGAGGAGTCC 303  
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 Qy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
 |||||  
 Db 304 AACATCACCATGCAGATTATCGGATCAAACTCACCAGGCCAGCACATAGGAGATG 363  
 |||||  
 Qy 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
 |||||  
 Db 364 AGCTTCCTACAGCACAAACAAATGTAATGCAGACCAAGAAAGATAGAGCAAGCAAGAA 423  
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 Qy 141 Lys 141  
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 Db 424 AAA 426

## RESULT 15

US-09-392-932-8  
 ; Sequence 8, Application US/09392932  
 ; Patent No. 6352975  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schreiner, George F.  
 ; TITLE OF INVENTION: METHODS OF TREATING HYPERTENSION AND  
 ; TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN  
 ; FILE REFERENCE: SCTOS 002A  
 ; CURRENT APPLICATION NUMBER: US/09/392,932  
 ; CURRENT FILING DATE: 1999-09-09  
 ; EARLIER APPLICATION NUMBER: 60/099,694  
 ; EARLIER FILING DATE: 1998-09-09  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: fastseq for Windows Version 4.0  
 ; SEQ ID NO 8  
 ; LENGTH: 576  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 US-09-392-932-8

Alignment Scores:  
 Pred. No.: 3.43e-92 Length: 576  
 Score: 787.00 Matches: 140  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 99.37% Indels: 0  
 DB: 4 Gaps: 0

US-09-884-050-2 (1-141) x US-09-392-932-8 (1-576)

Qy 1 MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20  
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 Db 1 ATGAACCTTCTGCTCTTGGTGATGGAGCCCTTGCTTGTCTGTCTACCTCCACCAT 60  
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 Qy 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluVal 40  
 |||||  
 Db 61 GCCAAGTGTCCAGGCTGCACCAATGCGCAGAGGAGGAGGAGCAATCATCACGAAGTG 120  
 |||||  
 Qy 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
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 Db 121 GTGAAGTTTCATGGATGTCTATCAGCGCAGCTACTGCCATCCAATCGAGACCCCTGGTGAC 180  
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QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
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Db 181 ATCTTCAGGAGTACCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTG 240  
QY 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
|||||  
Db 241 ATCGATGCGGGGCTGCTGCAATGACGAGGGCTGGAGTGTGTGCCCACTGAGGAGTCC 300  
QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
|||||  
Db 301 AACATCACCATGCAGATTATGCGGATCAAACTCACCAAGGCCAGCACATAGGAGAGATG 360  
QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
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Db 361 AGCTTCTACAGCACAAACAATGTGAATGCAGACCAAGAAAGATAGAGCAAGACAAGAA 420

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Job time : 68 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

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Perfect score: 426  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues  
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*  
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6: /SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*  
7: /SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.\*  
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19: /SID22/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.\*  
20: /SID22/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.\*  
21: /SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	425	99.8	495	AAZ29996	Nucleotide sequenc
2	425	99.8	627	AAZ29997	Nucleotide sequenc
3	422.8	99.2	516	AAV28396	Vascular endotheli
4	422.8	99.2	545	AAZ29999	Nucleotide sequenc
5	422.8	99.2	648	AAZ39835	Human A215 nucleot
6	422.8	99.2	648	AAC83521	Human VEGF C subun
7	422.8	99.2	666	AAZ29998	Nucleotide sequenc
8	422.8	99.2	1195	AAQ04474	Human vascular per
9	422.8	99.2	1195	AAZ90498	Human vascular end

10	422.4	99.2	444	21	AAZ93345	Human vascular end
11	422.4	99.2	444	21	AAZ99544	Nucleotide sequenc
12	422.4	99.2	444	22	AAC90473	Human vascular end
13	422.4	99.2	444	22	AAC90477	Human VEGF121 DNA
14	422.4	99.2	444	24	ABL57427	Human vascular end
15	422.4	99.2	473	15	AAQ99080	cDNA encoding huma
16	422.4	99.2	473	17	AAAT17613	VEGF121 coding seq
17	422.4	99.2	473	21	AAAT12853	cDNA encoding VEGF
18	422.4	99.2	544	22	AAH21876	Human VEGF splice
19	422.4	99.2	774	18	AAT85644	Antisense inhibito
20	422.4	99.2	774	18	AAT79139	Human vascular end
21	422.4	99.2	774	19	AAV15102	Human vascular end
22	422.4	99.2	774	19	AAZ93393	Human vascular end
23	422.4	99.2	1873	19	AAV15103	Human vascular end
24	422.4	99.2	1873	20	AAZ21568	Vascular endotheli
25	422	99.1	541	22	AAH26082	Vascular endotheli
26	422	99.1	573	22	AAZ24900	Nucleotide sequenc
27	422	99.1	576	24	AAZ31056	Human vascular end
28	422	99.1	576	24	ABL91778	Human polynucleoti
29	422	99.1	605	16	AAQ99081	cDNA encoding huma
30	422	99.1	605	17	AAAT17614	VEGF165 coding seq
31	422	99.1	605	21	AAAT12854	cDNA encoding VEGF
32	422	99.1	649	17	AAZ33609	Vascular endotheli
33	422	99.1	1395	17	AAZ35740	VEGF165-Alamet-SAP
34	422	99.1	4597	22	AAZ24901	Nucleotide sequenc
35	422	99.1	5610	21	AAZ75628	Nucleotide sequenc
36	422	99.1	5610	24	AAZ39240	pD10-VEGFuc vector
37	421.2	98.9	516	20	AAZ57724	Human VEGF(145) CO
38	421.2	98.9	516	21	AAZ93346	Human vascular end
39	421.2	98.9	516	21	AAZ99545	Nucleotide sequenc
40	421.2	98.9	516	22	AAC90478	Human VEGF145 DNA
41	421.2	98.9	516	24	ABL57428	Human vascular end
42	421.2	98.9	642	21	AAZ93348	Human vascular end
43	421.2	98.9	642	21	AAZ99547	Nucleotide sequenc
44	421.2	98.9	642	22	AAZ90480	Human VEGF189 DNA
45	421.2	98.9	642	24	ABL57430	Human vascular end

ALIGNMENTS

RESULT 1

AAZ29996  
ID AAZ29996 standard; cDNA; 495 BP.

XX AC AAZ29996;

XX XX 26-JAN-2000 (first entry)

DT XX Nucleotide sequence of VEGF-Al38 protein coding region.

DE XX Vascular endothelial factor; VEGF; VEGF-Al38: variant; vascular disease;  
KW cardiovascular disease; vascular cell proliferation; angioplasty;  
KW restenosis; drug permeation; tumour; ischemic condition;  
KW cardiac infarction; chronic coronary ischemia; stroke; wound treatment;  
KW chronic lower limb ischemia; peripheral vascular disease; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 1..495

FT FT /\*tag= a

FT FT /product= "VEGF-Al38"

FT FT sig\_peptide 1..78

FT FT /\*tag= b

FT FT /note= "secretion signal sequence"

FT FT exon 1..90

FT FT /\*tag= c

FT FT /number= 1

FT FT exon 91..118

FT FT /\*tag= d

FT FT /number= 2

FT FT exon 119..315







```
PI Thomas KA, Bayne ML;
XX WPI; 2000-038268/03.
DR P-PSDB; AAY57035.
XX
XX Purified and isolated vascular endothelial cell growth factor C subunit
PT for the induction of tissue repair or growth -
XX
XX Disclosure; Fig 12; 58pp; English.
XX
XX This is the nucleotide sequence of human A215, which is used in the
CC invention. The invention relates to a purified and isolated vascular
CC endothelial cell growth factor (VEGF) C subunit amino acid sequence
CC AAY57025. VEGF exists in various microheterogenous forms, and is useful
CC for the promotion of vascular development and repair. The invention also
CC relates to human VEGF heterodimers AC or BC and homodimer CC, where A, B
CC and C are subunit amino acid sequences. The VEGF AC, BC or CC amino acid
CC sequences can be used in a tissue repairing pharmaceutical composition.
CC The novel growth factors are useful for the production or coverage of
CC artificial blood vessels with vascular endothelial cell. They are also
CC useful for the induction of tissue growth and repair.
XX
XX Sequence 648 BP; 186 A; 155 C; 180 G; 127 T; 0 other;
SQ
Query Match 99.2%; Score 422.8; DB 21; Length 648;
Best Local Similarity 99.5%; Pred. No. 5.7e-118;
Matches 424; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGAATTTCTGCTGCTTGGGTGCATTTGGAGCCCTTGCTGCTCTTACCTCCACCAT 60
Db 1 ATGAATTTCTGCTGCTTGGGTGCATTTGGAGCCCTTGCTGCTCTTACCTCCACCAT 60
Qy 61 GCCAAGTGGTCCCAGGCTGCACCCATGCGAGAAGGAGGAGGCGAGAATCATCAGAAAGTG 120
Db 61 GCCAAGTGGTCCCAGGCTGCACCCATGCGAGAAGGAGGAGGCGAGAATCATCAGAAAGTG 120
Qy 121 GTGAAGTTTCATGGATGTTCTATCAGCGCAGCTACTGCCATCCAAATCGAGACCCCTGGTGGAC 180
Db 121 GTGAAGTTTCATGGATGTTCTATCAGCGCAGCTACTGCCATCCAAATCGAGACCCCTGGTGGAC 180
Qy 181 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCCATCTGTGTCGCCCTG 240
Db 181 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCCATCTGTGTCGCCCTG 240
Qy 241 ATGCGATCGGGGGCTGCTGCAATGACGAGGCGCTTGGAGTGTGTCGCCACTGAGGAGTCC 300
Db 241 ATGCGATCGGGGGCTGCTGCAATGACGAGGCGCTTGGAGTGTGTCGCCACTGAGGAGTCC 300
Qy 301 AACATCACCATGCAGATTATGCGGATCAAACTCACCAGGCCAGCAGCATAGGAGAGATG 360
Db 301 AACATCACCATGCAGATTATGCGGATCAAACTCACCAGGCCAGCAGCATAGGAGAGATG 360
Qy 361 AGCTTCCCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAAGATAGACAGCAAGAA 420
Db 361 AGCTTCCCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAAGATAGACAGCAAGAA 420
Qy 421 AAGTAA 426
Db 421 AAAAAA 426
RESULT 6
AAC83521
ID AAC83521 standard; cDNA; 648 BP.
XX
AC AAC83521;
XX
XX 26-FEB-2001 (first entry)
XX
XX Human VEGF C subunit coding sequence SEQ ID NO: 48.
XX
XX Vascular endothelial growth factor; VEGF C subunit; cell division;
KW artificial blood vessel; tissue growth; tissue repair; ss.
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XX Homo sapiens.
XX US6140073-A.
PN
XX 31-OCT-2000.
PD
XX 16-JAN-1996; 96US-0586039.
XX
XX 20-SEP-1993; 93US-0124259.
XX 28-MAR-1991; 91US-0676436.
XX (MERI ) MERCK & CO INC.
XX Thomas KA, Bayne ML;
XX WPI; 2001-014858/02.
XX P-PSDB; AAB37512.
XX
XX Human vascular endothelial cell growth factor (VEGF) C subunit DNA and
XX protein, useful for promoting vascular development and repair, and for
XX promoting tissue repair, especially for treating wounds in mammals -
XX
XX Disclosure; Fig 12; 58pp; English.
XX
XX The present invention is concerned with the human vascular endothelial
XX growth factor (VEGF) C subunit. VEGF is a vascular endothelial cell
XX mitogen and can be used to promote vascular development and repair. The C
XX subunit may exist as a homodimer or a heterodimer with the VEGF A or B
XX subunit. VEGF can be used in the treatment of wounds of mammals, to cover
XX artificial blood vessels with vascular endothelial cells, in the
XX production of artificial blood vessels and to induce tissue repair or
XX growth.
XX
XX Sequence 648 BP; 186 A; 155 C; 180 G; 127 T; 0 other;
SQ
Query Match 99.2%; Score 422.8; DB 22; Length 648;
Best Local Similarity 99.5%; Pred. No. 5.7e-118;
Matches 424; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGAATTTCTGCTGCTTGGGTGCATTTGGAGCCCTTGCTGCTCTTACCTCCACCAT 60
Db 1 ATGAATTTCTGCTGCTTGGGTGCATTTGGAGCCCTTGCTGCTCTTACCTCCACCAT 60
Qy 61 GCCAAGTGGTCCCAGGCTGCACCCATGCGAGAAGGAGGAGGCGAGAATCATCAGAAAGTG 120
Db 61 GCCAAGTGGTCCCAGGCTGCACCCATGCGAGAAGGAGGAGGCGAGAATCATCAGAAAGTG 120
Qy 121 GTGAAGTTTCATGGATGTTCTATCAGCGCAGCTACTGCCATCCAAATCGAGACCCCTGGTGGAC 180
Db 121 GTGAAGTTTCATGGATGTTCTATCAGCGCAGCTACTGCCATCCAAATCGAGACCCCTGGTGGAC 180
Qy 181 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCCATCTGTGTCGCCCTG 240
Db 181 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCCATCTGTGTCGCCCTG 240
Qy 241 ATGCGATCGGGGGCTGCTGCAATGACGAGGCGCTTGGAGTGTGTCGCCACTGAGGAGTCC 300
Db 241 ATGCGATCGGGGGCTGCTGCAATGACGAGGCGCTTGGAGTGTGTCGCCACTGAGGAGTCC 300
Qy 301 AACATCACCATGCAGATTATGCGGATCAAACTCACCAGGCCAGCAGCATAGGAGAGATG 360
Db 301 AACATCACCATGCAGATTATGCGGATCAAACTCACCAGGCCAGCAGCATAGGAGAGATG 360
Qy 361 AGCTTCCCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAAGATAGACAGCAAGAA 420
Db 361 AGCTTCCCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAAGATAGACAGCAAGAA 420
Qy 421 AAGTAA 426
Db 421 AAAAAA 426
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the treatment or prevention of diseases of the central nervous system associated with alterations in cerebrospinal fluid, e.g. stroke, meningitis, tumour, infections, and bone growth disorders; treatment or prevention of hypoxia or hypercapnia or fibrosis arising from accumulation of fluid secretions in the lungs, e.g. acute respiratory distress syndrome, toxic alveolar injury, pneumonia, infections, surgical intervention, cystic fibrosis; treatment or prevention of pulmonary dysfunction arising from injury to the pulmonary endothelium, including disorders arising from premature birth, and pulmonary hypertension; treatment or prevention of disease arising from disordered transport of fluid and solutes across the intestinal epithelium, e.g. inflammatory bowel disease, diarrhoea; treatment or prevention of ascites accumulation in the peritoneum; enhancement of efficacy of solute flux; preservation or enhancement of function of organ allografts; and treatment of cardiac valve disease. This sequence encodes the native human vascular endothelial growth factor hVEGF121. The activity of VEGF is mediated by interaction with specific receptors on target tissues, most notably the vascular endothelium. VEGF exists as five different length monomer chains due to alternative splicing of the VEGF RNA transcript. VEGF121 is unique among the five forms in that it does not bind to heparin like molecules associated with the extracellular matrix.

Sequence 444 BP: 121 A: 113 C: 122 G: 88 T: 0 other:

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Query Match      99.2%; Score 422.4; DB 21; Length 444;
Best Local Similarity 99.8%; Pred. No. 6.4e-118;
Matches 423: Conservative 0; Mismatches 1; Indels 0; Caps
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Qy	1	ATGAAC	TTTCTGCTGCTTGGGTG	CAATGGAGC	CTTGCCTT	GCTGCTCTACCTCC	ACCAT	60
Db	1	ATGAAC	TTTCTGCTGCTTGGGTG	CAATGGAGC	CTTGCCTT	GCTGCTCTACCTCC	ACCAT	60
Qy	61	GCCAA	GTGGTCCCAAGGCTGCAC	CCATGGC	AAGAGGAGG	GGCAGAA	TATCACGAAGTG	120
Db	61	GCCAA	GTGGTCCCAAGGCTGCAC	CCATGGC	AAGAGGAGG	GGCAGAA	TATCACGAAGTG	120
Qy	121	GTGNA	GTTCATGATGCTATCAG	CAGCAGCTACTG	CCATCCCA	TCCGAC	CTGGTGGAC	180
Db	121	GTGNA	GTTCATGATGCTATCAG	CAGCAGCTACTG	CCATCCCA	TCCGAC	CTGGTGGAC	180
Qy	181	ATCTT	CCAGGAGTACCTGATG	AGATCGAGTAC	ATCTTCA	AGCCATC	CTGTGTGCCCTTG	240
Db	181	ATCTT	CCAGGAGTACCTGATG	AGATCGAGTAC	ATCTTCA	AGCCATC	CTGTGTGCCCTTG	240
Qy	241	ATGCG	ATGCGGGGCTGCTGCA	TGACGAGG	GGCTGAG	TGTGTC	CCCACTGAGGAGTCC	300
Db	241	ATGCG	ATGCGGGGCTGCTGCA	TGACGAGG	GGCTGAG	TGTGTC	CCCACTGAGGAGTCC	300
Qy	301	AACAT	CACCATG	CAGATTATG	CGGATCA	AACCTC	ACCAAGGCCAGGCACATAGGAGAGATG	360
Db	301	AACAT	CACCATG	CAGATTATG	CGGATCA	AACCTC	ACCAAGGCCAGGCACATAGGAGAGATG	360
Qy	361	AGCTT	CTCTACAGCACACA	AAATGTG	GAATGC	AGACCA	AAAGAAAGATAGAGCAACACAAGAA	420
Db	361	AGCTT	CTCTACAGCACACA	AAATGTG	GAATGC	AGACCA	AAAGAAAGATAGAGCAACACAAGAA	420
Qy	421	AAAT	424					
Db	421	AAAT	424					

RESULT 11	
AAZ99544	
ID	AAZ99544 standard; DNA; 444 BP.
XX	
XX	
AC	AAZ99544;
XX	
XX	
DT	03-JUL-2000 (first entry)
XX	
XX	
DE	Nucleotide sequence of vascular endothelial growth factor 121.
XX	
XX	
KW	Human; vascular endothelial growth factor; VEGF 121; angiogenic factor

Novel methods for treating hypertension by administering a factor which increases angiogenesis and/or vascular permeability -

Claim 5; Figure 6; 5lpp; English.

Administering vascular endothelial growth factor (VGEF) can be used for treating hypertension (especially salt-dependent hypertension)

Administration of VGEF promotes angiogenesis and/or vascular or capillary permeability. The method is also useful in treating disorders related to abnormal transport of solutes across endothelial cells. Such disorders include the treatment or prevention of kidney disease associated with impaired filtration or excretion of solutes;



Db	61	GCCAAGTGGTCCGAGGCTGCACCCATGGCAGAAGGAGGGGAGGAATCATCAGGAATG	120
QY	121	GTGAAGTTTCATGATGCTATCAGCGCAGCTACTGCATCCAATCGAGACCCCTGGTGGAC	180
Db	121	GTGAAGTTTCATGATGCTATCAGCGCAGCTACTGCATCCAATCGAGACCCCTGGTGGAC	180
QY	181	ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTG	240
Db	181	ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTG	240
QY	241	ATGCGATCGGGGCTCTCTGCATGACGAGGGCTGGAGTGTGTGCCACTGAGGAGTCC	300
Db	241	ATGCGATCGGGGCTCTCTGCATGACGAGGGCTGGAGTGTGTGCCACTGAGGAGTCC	300
QY	301	AACATACCATCGAGATTATGCGGATCAAACTCCACCAAGCCAGCACATAGGAGAGATG	360
Db	301	AACATACCATCGAGATTATGCGGATCAAACTCCACCAAGCCAGCACATAGGAGAGATG	360
QY	361	AGCTTCTTACAGCACACAATAATGTGAATGCAGACCAAGAAAGATAGACGAACAAGAA	420
Db	361	AGCTTCTTACAGCACACAATAATGTGAATGCAGACCAAGAAAGATAGACGAACAAGAA	420
QY	421	AAAGT 424	
Db	421	AAAT 424	
RESULT 12			
AAC90473			
XX	ID	AAC90473 standard; cDNA; 444 BP.	
AC	AC	AAC90473;	
XX	XX		
DT	13-MAR-2001	(first entry)	
XX	XX	Human vascular endothelial growth factor cDNA.	
DE	DE		
XX	XX	Human; vascular endothelial growth factor; VEGF; VEGF dimer;	
KW	KW	hypertensive; litholytic; nephrotropic; antiarteriosclerotic;	
KW	KW	antiinflammatory; angiogenesis; vascular remodelling; injury; wound;	
KW	KW	peripheral arterial disease; coronary artery disease; hypoxia;	
KW	KW	essential hypertension; microvascular angiopathy; hypercapnia;	
KW	KW	polycystic kidney disease; vascular endothelial cell repair;	
KW	KW	lung disease; kidney disease; inflammatory bowel disease; ss.	
XX	XX		
OS	OS	Homo sapiens.	
XX	XX	WO200071716-A2.	
PN	PN	30-NOV-2000.	
PD	PD	18-MAY-2000; 2000WO-US13636.	
PF	PF	20-MAY-1999; 99US-0135312.	
XX	XX	20-JAN-2000; 2000US-0177407.	
PR	PR	(SCIO-) SCIOS INC.	
XX	XX	WPI: 2001-041064/05.	
XX	XX	P-PSDB; AAB50427, AAB50428.	
XX	XX	Vascular endothelial growth factor dimer, useful for treating essenti-	
XX	XX	hypertension, polycystic kidney diseases, microvascular angiopathy an	
XX	XX	coronary artery disease, comprising two monomeric subunits -	
XX	XX	Disclosure; Fig 1; 61pp; English.	
PS	PS		
XX	XX	The present sequence encodes a monomer of a vascular endothelial grow	
CC	CC	factor (VEGF) dimer. The dimer comprises a first and a second monomer	

	Query Match	99.2%	Score 422.4	DB 21	Length 444
	Best Local Similarity	99.8%	Pred. No. 6.4e-118		
	Matches 423	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	1	ATGAAC	TTTCGTGTCCTTGGGTGCATGTGGAGCCTTGCCTTGCCTCTACCTCCACCAT	60	
Db	1	ATGAAC	TTTCGTGTCCTTGGGTGCATGTGGAGCCTTGCCTTGCCTCTACCTCCACCAT	60	
QY	61	GCCAAGTGTG	TCCTCCAGGCTGCACCCATGGCAAGAGGAGGCGGACGAGATCATCAGGAAGTG	120	

PN	WO200071713-A1.
XX	
XX	
PD	30-NOV-2000.
XX	
XX	
PF	18-MAY-2000; 2000WO-US13536.
XX	
XX	
PR	20-MAY-1999; 99US-0135312.
XX	
XX	
PA	(SCIO-) SCIOS INC.
XX	
PI	Pollitt NS, Abraham JA;
XX	
XX	
DR	WPI; 2001-025162/03.

XX  
XX

PT replacing a Cys residue, for producing variant useful for treating hypertension, stroke, diabetes, lupus, glomerulonephritis, meningitis, PT tumor, pneumonia, infections -

XX	Disclosure; Fig 2; 62pp; English.	
XX		
CC	The present sequence is given in a specification relating to a method for	
CC	enhancing the biological activity of a vascular endothelial growth factor	
CC	(VEGF) originally having a cysteine residue at a position 116 of the 121	
CC	amino acid native mature human VEGF. The method comprises eliminating the	
CC	cysteine residue to produce a VEGF variant. The variant is useful for	
CC	inducing angiogenesis or vascular remodelling, for prevention or repair	
CC	of injury to blood vessels, where injury is associated with haemolytic	
CC	uraemic syndrome (HUS) or microvascular angiopathy such as thrombotic	
CC	microangiopathy (TMA). The VEGF variant is also useful for treatment of	
CC	essential hypertension in a patient. The variant is useful for treating	
CC	coronary artery disease and/or peripheral arterial disease, to foster	
CC	myocardial blood vessel growth and to improve blood flow to the heart. It	
CC	is useful for the treatment and prevention of kidney diseases associated	
CC	with injury to, or atrophy of, the vasculature of the glomerulus and	
CC	interstitium and for the treatment and prevention of acute renal failure,	
CC	myocardial infarction, ischaemic bowel disease, transient ischaemic	
CC	attacks, stroke, hypoxia, hypercapnia, focal glomerulosclerosis,	
CC	amyloidosis, glomerulonephritis, diabetes, systemic lupus erythematosus	
CC	or chronic hypoxia/atrophy. It is also useful in the preservation or	
CC	enhancement of function of organ allografts and xenografts, and for	
CC	treating disorders related to abnormal transport of solutes across	
CC	endothelial cells such as meningitis, tumour, infections, disorders of	
CC	bone growth, acute respiratory distress syndrome, toxic alveolar injury,	
CC	pneumonia, cystic fibrosis, inflammatory bowel disease, infectious	
CC	diarrhoea or cardiac valve disease.	
XX		
SQ	Sequence 444 BP; 121 A; 113 C; 122 G; 88 T; 0 other;	
	Query Match 99.2%; Score 422.4; DB 22; Length 444;	

Qy 1 ATGAACCTTCTGCTGTCTTGGGTGCATTGGAGCCCTTGCCCTTGCTGCTCTACCTCCACCAT 60

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**TOTAL**

**TOTAL TO**

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Qy		
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Db		





GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model  
Run on: November 20, 2002, 01:17:26 ; Search time 2685 Seconds  
(without alignments)  
4617.428 Million cell updates/sec  
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Gapop 10.0 , Gapext 1.0  
Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
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Maximum Match 100%  
Listing first 45 summaries

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- 2: gb\_hgt.\*
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- 6: gb\_pat.\*
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- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_or.\*
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- 22: em\_pat.\*
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- 25: em\_ro.\*
- 26: em\_sts.\*
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- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	422.8	99.2	630	9	HSA010438	AJ010438 Homo sapi
2	422.8	99.2	648	6	AR117116	AR117116 Sequence
3	422.8	99.2	1195	9	HUMVDF	M27281 Human vascu
4	422.4	99.2	444	6	AR198591	AR198591 Sequence
5	422.4	99.2	444	6	AX048686	AX048686 Sequence
6	422.4	99.2	444	6	AX050391	AX050391 Sequence
7	422.4	99.2	444	6	AF214570	AF214570 Homo sapi
8	422.4	99.2	544	6	E49139	E49139 Human large
9	422.4	99.2	774	6	AR118875	AR118875 Sequence
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11	422.4	99.2	774	6	E13215	E13215 Human mRNA
12	422.4	99.2	774	6	E13332	E13332 cDNA encod1
13	422.4	99.2	774	6	E14233	E14233 Human mRNA
14	422.4	99.2	774	6	E15156	E15156 Human VEGF
15	422.4	99.2	1873	6	E15157	E15157 Human VEGF
16	422.4	99.2	1873	6	E22645	E22645 Antisense n
17	422	99.1	541	6	AX204783	AX204783 Sequence
18	422	99.1	541	9	AF091352	AF091352 Homo sapi
19	422	99.1	573	6	AX060342	AX060342 Sequence
20	422	99.1	576	6	AX481507	AX481507 Sequence
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22	422	99.1	576	9	AF486837	AF486837 Homo sapi
23	422	99.1	606	9	AF430806	AF430806 Homo sapi
24	422	99.1	649	9	HSVEGF	X62568 H. sapiens v
25	422	99.1	4597	6	AX060344	AX060344 Sequence
26	422	99.1	5610	6	AX411805	AX411805 Sequence
27	421.2	98.9	516	6	AR198592	AR198592 Sequence
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31	421.2	98.9	642	6	AX050397	AX050397 Sequence
32	421.2	98.9	699	6	AR198595	AR198595 Sequence
33	421.2	98.9	699	6	AX050399	AX050399 Sequence
34	421.2	98.9	815	6	AX234496	AX234496 Sequence
35	421.2	98.9	815	9	S85192	S85192 Homo sapien
36	420.4	98.7	576	6	A64392	A64392 Sequence 5
37	420.4	98.7	576	6	AR198593	AR198593 Sequence
38	420.4	98.7	576	6	AX050395	AX050395 Sequence
39	420.4	98.7	640	9	AY047581	AY047581 Homo sapi
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42	420.4	98.7	990	6	AX234351	AX234351 Sequence
43	420.4	98.7	990	6	AX409689	AX409689 Sequence
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ALIGNMENTS

RESULT 1  
HSA010438  
LOCUS  
DEFINITION Homo sapiens mRNA for vascular endothelial growth factor, splicing  
variant VEGF183.  
ACCESSION AJ010438  
VERSION AJ010438.1 GI:3647280  
KEYWORDS vascular endothelial growth factor; vegf gene; VEGF183 protein.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 630)  
AUTHORS Pei,D.  
TITLE Direct Submission





/protein\_id="CAC21760.1"  
 /db\_xref="GI:12225841"  
 /translation="MNFLLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFM  
 DVYQSYCHPIETLVDIFQEPDEIEYIFKPSVPLMRGCGCNDGLEGVPTESNI  
 TMOIMRIKHQGHIGEMSFLOHNKCECRPKDRARQKDKPRR"  
 BASE COUNT 121 a 113 c 122 g 88 t  
 ORIGIN

Query Match 99.2%; Score 422.4; DB 6; Length 444;  
 Best Local Similarity 99.8%; Pred. No. 1.8e-103;  
 Matches 423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ATGAACATTTCTGCTTGGTGCATTTGGAGCCTTGCCTTGTCTACCTCCACCAT 60  
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 QY 421 AAGT 424  
 Db 421 AAAT 424

RESULT 6  
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 LOCUS AX050391 1 from Patent WO0071713. 444 bp DNA linear PAT 12-JAN-2001  
 DEFINITION Sequence  
 ACCESSION AX050391  
 VERSION AX050391.1 GI:12226615  
 KEYWORDS  
 SOURCE human.  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 AUTHORS Pollitt,N.S. and Abraham,J.A.  
 TITLE Vascular endothelial growth factor variants  
 JOURNAL Patent: WO 0071713-A 1 30-NOV-2000;  
 SCIOS INC. (US)

FEATURES  
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BASE COUNT 121 a 113 c 122 g 88 t  
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 Best Local Similarity 99.8%; Pred. No. 1.8e-103;  
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 Db 361 AGCTTCCTACAGCACACAAATGTGAATGCAGACCAAGAAAGATAGACACAAGAA 420  
 QY 421 AAGT 424  
 Db 421 AAAT 424

RESULT 7  
 AF214570  
 LOCUS AF214570 1 from Patent WO0071713. 444 bp mRNA linear PRI 23-DEC-1999  
 DEFINITION Homo sapiens vascular endothelial growth factor isoform 121  
 precursor, mRNA, complete cds.  
 ACCESSION AF214570  
 VERSION AF214570.1 GI:6631028  
 KEYWORDS  
 SOURCE Homo sapiens.  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 AUTHORS Sato,J.D. and Whitney,R.G.  
 TITLE Human cDNA for vascular endothelial growth factor isoform VEGF121  
 JOURNAL unpublished  
 REFERENCE  
 AUTHORS Sato,J.D. and Whitney,R.G.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-DEC-1999) Division of Cell, Molecular and  
 Developmental Biology, American Type Culture Collection, 10801  
 University Boulevard, Manassas, VA 20110, USA

FEATURES  
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 /organism="Homo sapiens"  
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 precursor"  
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QY 421 AAGT 424  
Db 521 AAAT 524

RESULT 10  
E11017  
LOCUS E11017 774 bp RNA linear PAT 29-SEP-1997  
DEFINITION A part of p8u 2 including vascular endothelial cell growth factor (VEGF) structural gene.  
ACCESSION E11017  
VERSION E11017.1 GI:22024658  
KEYWORDS JP 1996070899-A/1.  
SOURCE unidentified.  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 774)  
AUTHORS Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.  
TITLE METHOD FOR SEARCHING ANTISENSE NUCLEIC ACID  
JOURNAL Patent: JP 1996070899-A 1 19-MAR-1996;  
TOAGOSEI CO LTD  
COMMENT OS Unknown  
PN JP 1996070899-A/1  
PD 19-MAR-1996  
PF 11-NOV-1994 JP 94P 145146  
PR 27-JUN-1994 JP 94P 145146  
PI UCHIDA KIYOSHI, UCHIDA TARAYOSHI, TANAKA YOICHI, MATSUDA YOKO, KONDO SHINICHI  
PC C1201/68,C12N15/09,G01N33/50;  
CC strandedness: Single;  
CC topology: Linear;  
FH Key Location/Qualifiers  
FT source 1. .774 /organism='Unclassified'.  
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BASE COUNT 221 a 193 c 200 g 160 t  
ORIGIN

Query Match 99.2%; Score 422.4; DB 6; Length 774;  
Best Local Similarity 99.8%; Pred. No. 1.8e-103;  
Matches 423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAACCTTCTGCTGCTTGGGTGCATTTGGAGCCTTGCCTTGTCTACCTCCACCAT 60  
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QY 361 AGCTTCTACAGCACAAATGTGAATGCGAGCCAAAGAAAGATAGAGCAAGACAAAGAA 420  
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QY 421 AAGT 424  
Db 521 AAAT 524

RESULT 11  
E13215  
LOCUS E13215 774 bp DNA linear PAT 27-APR-1998  
DEFINITION Human mRNA for vascular endothelial cell growth factor.  
ACCESSION E13215  
VERSION E13215.1 GI:3252020  
KEYWORDS JP 1997154579-A/1.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 774)  
AUTHORS Matsuda,Y. and Uchida,K.  
TITLE PREPARATION OF ANTISENSE NUCLEIC ACID  
JOURNAL Patent: JP 1997154579-A 1 17-JUN-1997;  
TOAGOSEI CO LTD  
COMMENT OS Homo sapiens (human)  
PN JP 1997154579-A/1  
PD 17-JUN-1997  
PF 05-JUL-1996 JP 1996195419  
PR 03-OCT-1995 JP 95P 279752  
PI MATSUDA YOKO, UCHIDA KIYOSHI  
PC C12N15/09,C07H21/02,C07H21/04//C12Q1/68;  
CC strandedness: Double;  
CC topology: Linear;  
FH Key Location/Qualifiers  
FT source 1. .774 /organism='Homo sapiens'.  
FT Location/Qualifiers  
1. .774 /organism='Homo sapiens' /db\_xref='taxon:9606'  
BASE COUNT 221 a 193 c 200 g 160 t  
ORIGIN

Query Match 99.2%; Score 422.4; DB 6; Length 774;  
Best Local Similarity 99.8%; Pred. No. 1.8e-103;  
Matches 423; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAACCTTCTGCTGCTTGGGTGCATTTGGAGCCTTGCCTTGTCTACCTCCACCAT 60  
Db 101 ATGAACCTTCTGCTGCTTGGGTGCATTTGGAGCCTTGCCTTGTCTACCTCCACCAT 160



100



**THIS PAGE BLANK (USPTO)**

Result No.	score	Query		Length	DB	ID	Description
		Match	%				
1	422	99.1	576	10	US-09-932-451A-1		Sequence 1, Appli
2	422	99.1	649	10	US-09-349-954A-1		Sequence 1, Appli
3	422	99.1	649	10	US-09-307-007-1		Sequence 1, Appli
4	422	99.1	1736	12	US-10-044-090-164		Sequence 164, App
5	422	99.1	3583	9	US-09-981-353-185		Sequence 185, App
6	421.2	98.9	516	10	US-09-812-133-1		Sequence 1, Appli
7	421.2	98.9	815	10	US-09-795-006A-146		Sequence 146, App
8	420.4	98.7	480	10	US-09-365-029-93		Sequence 93, Appl
9	420.4	98.7	990	10	US-09-980-107-2336		Sequence 93, Appl
10	420.4	98.7	990	10	US-09-795-006A-1		Sequence 2336, Ap
c	11	388.4	91.2	459	US-09-867-701-10298		Sequence 1, Appli
	12	367.4	86.2	2361	US-09-925-299-154		Sequence 10298, A
	13	271.8	63.8	388	US-09-795-006A-42		Sequence 154, App
	14	237.2	55.7	322	US-09-795-006A-50		Sequence 42, Appl
	15	233.4	54.8	388	US-09-795-006A-52		Sequence 50, Appl
16	228.4	53.6	391	10	US-09-795-006A-82		Sequence 54, Appl
17	223.6	52.5	391	10	US-09-795-006A-86		Sequence 82, Appl
18	210	49.3	322	10	US-09-795-006A-58		Sequence 86, Appl
19	206.2	48.4	388	10	US-09-795-006A-52		Sequence 58, Appl

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Db 121 GTCAAGTTCATGATGCTATACAGCGAGCTACTGCCATCCATCGAGACCCCTGGTGGAC 180
QY 181 ATCTTCAGAGGTACCCCTGATGATGAGTCGAGTACATCTTCAAGCCATCCTGTGTGCCCTTG 240
Db 181 ATCTTCAGAGGTACCCCTGATGATGAGTCGAGTACATCTTCAAGCCATCCTGTGTGCCCTTG 240
QY 241 ATCGGATGCGGGGGCTGCTCAATGACGAGGGGCTGGAGTGTGTGCCCACTGAGGAGTCC 300
Db 241 ATCGGATGCGGGGGCTGCTCAATGACGAGGGGCTGGAGTGTGTGCCCACTGAGGAGTCC 300
QY 301 AACATCACCATGCGAGATTATGCGGATCAAACTTCAACAGGCCAGCACATAGGAGAGATG 360
Db 301 AACATCACCATGCGAGATTATGCGGATCAAACTTCAACAGGCCAGCACATAGGAGAGATG 360
QY 361 AGCTTCTACAGCACACAATAATGTGAATGCAGACCAACAAAGATAGAGCAACACAAGAA 420
Db 361 AGCTTCTACAGCACACAATAATGTGAATGCAGACCAACAAAGATAGAGCAACACAAGAA 420
QY 421 AA 422
Db 421 AA 422
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RESULT 2
US-09-349-954A-1
; Sequence 1, Application US/09349954A
; Patent No. US20020019027A1
; GENERAL INFORMATION:
; APPLICANT: Hayward, Nicholas K.
; APPLICANT: Weber, Gunther
; APPLICANT: Grimmond, Sean
; APPLICANT: Larsson, Catharina
; TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
; FILE REFERENCE: SAME
; CURRENT APPLICATION NUMBER: US/09/349,954A
; CURRENT FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 08/765,588
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 649
; TYPE: DNA
; ORGANISM: Nucleotide Sequence of VEGF165
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17)..(589)
US-09-349-954A-1
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Query Match 99.1%; Score 422; DB 10; Length 649;
Best Local Similarity 100.0%; Pred. No. 3.1e-120;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAACCTTCTGCTGCTTGGTGCATTCGAGGCTTGCCTTGTCTGCTTCTACCTCCACCAT 60
Db 17 ATGACCTTCTGCTGCTTGGTGCATTCGAGGCTTGCCTTGTCTGCTTCTACCTCCACCAT 76

QY 61 GCCAAGTGTGCCAGGCTGCACCCATGGCAGAGAGGAGGCGGAGATATCATCAGGAAGTG 120
Db 77 GCCAAGTGTGCCAGGCTGCACCCATGGCAGAGAGGAGGCGGAGATATCATCAGGAAGTG 136

QY 121 GTGAAGTTCATGGATGCTCTATCAGCGCAGCTACTGCCATCCAATCGAGACCCCTGGTGGAC 180
Db 137 GTGAAGTTCATGGATGCTCTATCAGCGCAGCTACTGCCATCCAATCGAGACCCCTGGTGGAC 196

QY 181 ATCTTCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTTG 240
Db 197 ATCTTCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTTG 256

QY 241 ATCGGATGCGGGGGCTGCTCAATGACGAGGGGCTGGAGTGTGTGCCCACTGAGGAGTCC 300
Db 257 ATCGGATGCGGGGGCTGCTCAATGACGAGGGGCTGGAGTGTGTGCCCACTGAGGAGTCC 316

QY 301 AACATCACCATGCGAGATTATGCGGATCAAACTTCAAGCCATCCTGTGTGCCCTTG 360
Db 317 AACATCACCATGCGAGATTATGCGGATCAAACTTCAAGCCATCCTGTGTGCCCTTG 376

QY 421 ATCGGATGCGGGGGCTGCTCAATGACGAGGGGCTGGAGTGTGTGCCCACTGAGGAGTCC 420
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Db 257 ATCGGATGCGGGGGCTGCTCAATGACGAGGGGCTGGAGTGTGTGCCCACTGAGGAGTCC 316
QY 301 AACATCACCATGCGAGATTATGCGGATCAAACTTCAACAGGCCAGCACATAGGAGAGATG 360
Db 317 AACATCACCATGCGAGATTATGCGGATCAAACTTCAACAGGCCAGCACATAGGAGAGATG 376
QY 361 AGCTTCTACAGCACACAATAATGTGAATGCAGACCAACAAAGATAGAGCAACACAAGAA 420
Db 377 AGCTTCTACAGCACACAATAATGTGAATGCAGACCAACAAAGATAGAGCAACACAAGAA 436
QY 421 AA 422
Db 437 AA 438

RESULT 3
US-09-907-007-1
; Sequence 1, Application US/09907007
; Patent No. US20020142395A1
; GENERAL INFORMATION:
; APPLICANT: Hayward, Nicholas K.
; APPLICANT: Weber, Gunther
; APPLICANT: Grimmond, Sean
; APPLICANT: No. US20020142395A1denskjold, Magnus
; APPLICANT: Larsson, Catharina
; TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
; FILE REFERENCE: DAVIES
; CURRENT APPLICATION NUMBER: US/09/907,007
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 08/765,588
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 649
; TYPE: DNA
; ORGANISM: Nucleotide Sequence of VEGF165
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17)..(589)
US-09-907-007-1
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Query Match 99.1%; Score 422; DB 10; Length 649;
Best Local Similarity 100.0%; Pred. No. 3.1e-120;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGAACCTTCTGCTGCTTGGTGCATTCGAGGCTTGCCTTGTCTGCTTCTACCTCCACCAT 60
Db 17 ATGAACCTTCTGCTGCTTGGTGCATTCGAGGCTTGCCTTGTCTGCTTCTACCTCCACCAT 76

QY 61 GCCAAGTGTGCCAGGCTGCACCCATGGCAGAGAGGAGGCGGAGATATCATCAGGAAGTG 120
Db 77 GCCAAGTGTGCCAGGCTGCACCCATGGCAGAGAGGAGGCGGAGATATCATCAGGAAGTG 136

QY 121 GTGAAGTTCATGGATGCTCTATCAGCGCAGCTACTGCCATCCAATCGAGACCCCTGGTGGAC 180
Db 137 GTGAAGTTCATGGATGCTCTATCAGCGCAGCTACTGCCATCCAATCGAGACCCCTGGTGGAC 196

QY 181 ATCTTCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTTG 240
Db 197 ATCTTCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTTG 256

QY 241 ATCGGATGCGGGGGCTGCTCAATGACGAGGGGCTGGAGTGTGTGCCCACTGAGGAGTCC 300
Db 257 ATCGGATGCGGGGGCTGCTCAATGACGAGGGGCTGGAGTGTGTGCCCACTGAGGAGTCC 316

QY 301 AACATCACCATGCGAGATTATGCGGATCAAACTTCAAGCCAGCCAGCACATAGGAGAGATG 360
Db 317 AACATCACCATGCGAGATTATGCGGATCAAACTTCAAGCCAGCCAGCACATAGGAGAGATG 376

QY 361 AGCTTCTACAGCACACAATAATGTGAATGCAGACCAACAAAGATAGAGCAACACAAGAA 420
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Db 377 ACCTTCCTACAGCAACAATAATGTGAATGCAGCAACAAAGAAATAGAGCAAGCAAGAA 436  
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Qy 421 AA 422

Db 437 AA 438

## RESULT 4

US-10-044-090-164  
; Sequence 164, Application US/10044090  
; Patent No. US20020137081A1  
; GENERAL INFORMATION:  
; APPLICANT: Olga Bandman  
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION  
; FILE REFERENCE: PA-0028 US  
; CURRENT APPLICATION NUMBER: US/10/044,090  
; CURRENT FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 850  
; SOFTWARE: PERL Program  
; SEQ ID NO 164  
; LENGTH: 1736  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No. US20020137081A1 3348156CB1  
; NAME/KEY: unsure  
; LOCATION: 1434, 1438-1439, 1512, 1514, 1521-1522, 1530  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-044-090-164

Query Match 99.1%; Score 422; DB 12; Length 1736;

Best Local Similarity 100.0%; Pred. No. 5e-120;

Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACCTTCTGCTGCTGCTGGTGGTGCATTGGAGCCCTTGCCCTGCTGCTCTACCTCCACCAT 60  
|||||

Db 150 ATGAACCTTCTGCTGCTGCTGGTGGTGCATTGGAGCCCTTGCCCTGCTGCTCTACCTCCACCAT 209  
|||||

Qy 61 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAAAGAGGAGGCGCAGAATCATCACGAAGTG 120  
|||||

Db 210 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAAAGAGGAGGCGCAGAATCATCACGAAGTG 269  
|||||

Qy 121 GTGAAGTTCATGGATGCTCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCCCTGGTGAC 180  
|||||

Db 270 GTGAAGTTCATGGATGCTCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCCCTGGTGAC 329  
|||||

Qy 181 ATCTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTTAAGCCCATCTGCTGCGCCCTG 240  
|||||

Db 330 ATCTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTTAAGCCCATCTGCTGCGCCCTG 389  
|||||

Qy 241 ATGCGATGGGGGCTGCTGCAATACGAGGCGCTGGAGTGTGCGCCACTGAGGAGTCC 300  
|||||

Db 390 ATGCGATGGGGGCTGCTGCAATACGAGGCGCTGGAGTGTGCGCCACTGAGGAGTCC 449  
|||||

Qy 301 AACATCACCATGCAGATTATGGGATCAAACTCACCAGGCGCAGACATAGGAGAGTG 360  
|||||

Db 450 AACATCACCATGCAGATTATGGGATCAAACTCACCAGGCGCAGACATAGGAGAGTG 509  
|||||

Qy 361 AGCTTCCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAATAGAGCAAGCAAGAA 420  
|||||

Db 510 AGCTTCCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAATAGAGCAAGCAAGAA 569  
|||||

Qy 421 AA 422

Db 570 AA 571

## RESULT 5

US-09-981-353-185  
; Sequence 185, Application US/09981353  
; Patent No. US20020160382A1

; GENERAL INFORMATION:  
; APPLICANT: Lasek, Amy W.  
; APPLICANT: Jones, David A.  
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER  
; FILE REFERENCE: PA-0038 US  
; CURRENT APPLICATION NUMBER: US/09/981,353  
; CURRENT FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PERL Program  
; SEQ ID NO 185  
; LENGTH: 3583  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No. US20020160382A1 1384719.3  
; NAME/KEY: unsure  
; LOCATION: 3245, 3265  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-981-353-185

Query Match 99.1%; Score 422; DB 9; Length 3583;

Best Local Similarity 100.0%; Pred. No. 7e-120;

Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAACCTTCTGCTGCTGCTGGTGGTGCATTGGAGCCCTTGCCCTGCTGCTCTACCTCCACCAT 60  
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Db 1086 ATGAACCTTCTGCTGCTGCTGGTGGTGCATTGGAGCCCTTGCCCTGCTGCTCTACCTCCACCAT 1145  
|||||

Qy 61 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAAAGAGGAGGCGCAGAATCATCACGAAGTG 120  
|||||

Db 1146 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAAAGAGGAGGCGCAGAATCATCACGAAGTG 1205  
|||||

Qy 121 GTGAAGTTCATGGATGCTCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCCCTGGTGAC 180  
|||||

Db 1206 GTGAAGTTCATGGATGCTCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCCCTGGTGAC 1265  
|||||

Qy 181 ATCTTCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCCATCTGCTGCGCCCTG 240  
|||||

Db 1266 ATCTTCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCCATCTGCTGCGCCCTG 1325  
|||||

Qy 241 ATGCGATGGGGGCTGCTGCAATACGAGGCGCTGGAGTGTGCGCCACTGAGGAGTCC 300  
|||||

Db 1326 ATGCGATGGGGGCTGCTGCAATACGAGGCGCTGGAGTGTGCGCCACTGAGGAGTCC 1385  
|||||

Qy 301 AACATCACCATGCAGATTATGGGATCAAACTCACCAGGCGCAGACATAGGAGAGTG 360  
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Db 1386 AACATCACCATGCAGATTATGGGATCAAACTCACCAGGCGCAGACATAGGAGAGTG 1445  
|||||

Qy 361 AGCTTCCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAATAGAGCAAGCAAGAA 420  
|||||

Db 1446 AGCTTCCTACAGCAACAATAATGTGAATGCAGACCAAAAGAAATAGAGCAAGCAAGAA 1505  
|||||

Qy 421 AA 422

Db 1506 AA 1507

## RESULT 6

US-09-812-133-1

; Sequence 1, Application US/09812133

; Patent No. US20020065240A1

; GENERAL INFORMATION:

; APPLICANT: Thomas, Kenneth A., Jr.

; APPLICANT: Kendall, Richard L.

; APPLICANT: Bett, Andrew J.

; APPLICANT: Huckle, William R.

; TITLE OF INVENTION: GENE THERAPY FOR STIMULATION OF

; FILE REFERENCE: 2007P

; CURRENT APPLICATION NUMBER: US/09/812,133

; CURRENT FILING DATE: 2001-03-19

; PRIOR APPLICATION NUMBER: PCT/US98/22668





Db	417	AGCTTCTACAGCACACAAATGTGAATGCAGAGCAACAAAGATAGAGCAGACACAAGAA	476
Qy	421	AA	422
Db	477	AA	478

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RESULT 11
US-09-867-701-10298/c
; Sequence 10298, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; OF INVENTION: AND DIAGNOSIS OF OVA
; FILE REFERENCE: 210121.457
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10298
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(459)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-10298

```

Query Match	91.2%;	Score 388.4;	DB 10;	Length 459;	
Best Local Similarity	96.4%;	Pred. No. 5.6e-110;			
Matches 407;	Conservative 0;	Mismatches 13;	Indels 2;	Gaps 1;	
QY	1	ATGAACATTTCTGCTGCTCTTGGTGCAATGGAGCCCTTGCTTGCCTGCTCTACTCCACCAT	60		
Db	422	ATGAACATTNTGCTGTCTTGGTGCAATGGAGCCCTTGCTTGTGCTCTACTCCACCAT	363		
QY	61	GCCAAAGTGGTCCCAGGCTGCACCCATGGCAGAAGGAGGAGGCGCAAAATCATCAGAAAGTG	120		
Db	362	GCCAAAGTGGTCCCAGGCTGCACCCATGGCAGAAGGAGGAGGCGCAATCATCAGAAAGTG	303		
QY	121	GTGAAGTTCATGGATGCTATCAGCGGAGCTACTGCGCATCCAAATCGAGACCCCTGGTGGAC	180		
Db	302	GTGAAGTTCATGGATGCTATCAGCGGAGCTACTGCGCATCCAAATCGAGACCCCTGGTGGAC	243		
QY	181	ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCCATCCTGTGTGCCCTGT	240		
Db	242	ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCCATCCTGTGTGCCCTGT	183		
QY	241	ATGCGGATCGGGGGCTGCTGCAATGACGAGGGCCCTGGA--GTGTTGTCGCCACTGAGGAGT	298		
Db	182	ATGCGATGCGGGGGCTGCTGCAATGACGAGGGCCCTGAGTGTGTGCCACTGAGGAGT	123		
QY	299	CCAAATCACCATTGCAGATTATGGGATCAAACCTCACCAGGCGCAGCACATAGGAGAGA	358		
Db	122	CCAAATCACCATTGCAGATTATGGGATCAAACCTCACCAGGCGCAGCACATAGGAGAGA	63		
QY	359	TGAGCTTCCTACAGCACAAACAATGTGAATGCGAGACAAAGAAGATAGACGAAGCAAG	418		
Db	62	TGAGCTTCCTACAGCCCAACAATGTGAATGCGAGACAAAGAAGATAGACGAAGCAAG	3		
QY	419	AA 420			
Db	2	AA 1			

RESULT 12  
US-09-925-299-154  
; Sequence 154, Application US/09925299  
; Patent No. US20020055627A1

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: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA102
: CURRENT APPLICATION NUMBER: US/09/925,299
: CURRENT FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05883
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/134,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 1556
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 154
: LENGTH: 2361
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (92)
: OTHER INFORMATION: n equals a.t.g, or c
US-09-925-299-154

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Query Match	86.2%	Score 367.4	DB 10	Length 2361
Best Local Similarity	98.7%	Pred. No. 3.5e-103		
Matches 391	Conservative 0	Mismatches 2	Indels 3	Gaps 2
QY	29	GGAGCGTTGCGCTTGCTGTCTACCTCCACCATTGCCAAGTGGTCCCAAGGCTGCACCGCTGCACCCATGG	88	
Db	1	GGAGCGTTGCGCTTGCTGTCTACCTCCACCATTGCCAAGTGGTCCCAAGGCTGCACCCATGG	60	
QY	89	CAGAAAGGAGGGGCGAGAAATCATCACGAAGTGGTGAAGTTTCATGGATGCTCTATCAGCGCA	148	
Db	61	CAGAAAGGAGGGGCGAGAAATCATCACGAAG-GNTGAAGTTCATGGATGCTCTATCAGCGCA	119	
QY	149	GCTACTGCCATCCCAATCCGAGACCCGTGTGACATCTTCCAGGAGTACCCGTATGAGATCG	208	
Db	120	--TACTGCCATCCCAATCGAGACCCGTGTGACATCTTCCAGGAGTACCCGTATGAGATCG	177	
QY	209	AGTACATCTTCAAGCCATCTCTGTGTGCCCTGATGCGATCGCGGGGCTGCTCGCAATGACG	268	
Db	178	AGTACATCTTCAAGCCATCTCTGTGTGCCCTGATGCGATCGCGGGGCTGCTCGCAATGACG	237	
QY	269	AGGGCTCGAGTGTGTGCCCACTGAGAGTCCAACATCACCATGACAGATTATGCGGATCA	328	
Db	238	AGGGCTCGAGTGTGTGCCCACTGAGAGTCCAACATCACCATGACAGATTATGCGGATCA	297	
QY	329	AACCTCACRAGGCCAGCATATAGGAGAGTACGCTTCCACAGCACACAACAAATCTGAAAT	388	
Db	298	AACCTCACRAGGCCAGCATATAGGAGAGTACGCTTCCACAGCACACAACAAATCTGAAAT	357	
QY	398	GCAGACCAAGAAGATAGAGCAAGACAAGAAAGT	424	
Db	358	GCAGACCAAGAAGATAGAGCAAGACAAGAAAT	393	

RESULT 13  
US-09-795-006A-42  
Sequence 42, Application US/09795006A  
Patent No. US20020151680A1  
GENERAL INFORMATION:  
APPLICANT: Alitalo et al  
TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR  
TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS  
FILE REFERENCE: 28967/35977B  
CURRENT APPLICATION NUMBER: US/09/795, 006A  
CURRENT FILING DATE: 2001-02-26  
PRIOR APPLICATION NUMBER: US 60/205,331  
PRIOR FILING DATE: 2000-05-18  
PRIOR APPLICATION NUMBER: US 60/185,205  
PRIOR FILING DATE: 2000-02-25  
NUMBER OF SEQ ID NOS: 175  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 42

; LENGTH: 388  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Hybrid DNA  
; NAME/KEY: CDS  
; LOCATION: (8)..(385)  
US-09-795-006A-42

Query Match 63.8%; Score 271.8; DB 10; Length 388;  
Best Local Similarity 90.1%; Pred. No. 3.6e-74;  
Matches 291; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 100 GGGCAGATCATCAGCAAGTGGTGAAGTTCATGATGCTATCAGCGCAGCTACTGCCAT 159  
Db 8 GGGCAGATCATCAGCAAGTGGTGAAGTTCATGATGCTATCAGCGCAGCTACTGCCAT 67

QY 160 CCAATCGAGACCTGGTGGACATCTTCAGGAGTACCCTGATGAGATCGAGTACATCTTC 219  
Db 68 CCGATCGAGACCTGGTGGACATCTTCAGGAGTACCCTGATGAGATCGAGTACATCTTC 127

QY 220 AAGCCATCTGTGCCCTGTGATGCGGAGTCCCAACATCAGATTCGCGATCAACCTCACC 339  
Db 188 TCGTTCGCCAGGAGTCCCAACATCAGATTCGCGATCAACCTCACC 247

QY 340 GGGCAGCAGATAGGAGATGAGTCTTCTCCAGCAGTACAGCAACAATGTGAATGCGAGCA 399  
Db 248 GGGCAGCAGATCGGAGATGAGTCTTCTCCAGCAGTACAGCAACAATGTGAATGCGAGCA 307

QY 400 AAGATGAGCAAGCAAGAAA 422  
Db 308 AAGATGAGCAAGCAAGAAA 330

RESULT 14  
US-09-795-006A-50  
; Sequence 50, Application US/09795006A  
; Patent No. US20020151680A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo et al  
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR  
; FILE REFERENCE: 28967/35977B  
; CURRENT APPLICATION NUMBER: US/09/795,006A  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: US 60/205,331  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: US 60/185,205  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 50  
; LENGTH: 322  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: hybrid DNA  
; NAME/KEY: CDS  
; LOCATION: (8)..(322)  
US-09-795-006A-50

Query Match 55.7%; Score 237.2; DB 10; Length 322;  
Best Local Similarity 85.9%; Pred. No. 1.4e-63;  
Matches 263; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 100 GGGCAGATCATCAGCAAGTGGTGAAGTTCATGATGCTATCAGCGCAGCTACTGCCAT 159  
Db 8 GGGCAGATCATCAGCAAGTGGTGAAGTTCATGATGCTATCAGCGCAGCTACTGCCAT 67

QY 160 CCAATCGAGACCTGGTGGACATCTTCAGGAGTACCCTGATGAGATCGAGTACATCTTC 219  
Db 68 CCGATCGAGACCTGGTGGACATCTTCAGGAGTACCCTGATGAGATCGAGTACATCTTC 127

QY 220 AAGCCATCTGTGCCCTGTGATGCGGAGTCCCAACATCAGATTCGCGATCAACCTCACC 339  
Db 188 TCGTTCGCCAGGAGTCCCAACATCAGATTCGCGATCAACCTCACC 247

QY 340 GGGCAGCAGATAGGAGATGAGTCTTCTCCAGCAGTACAGCAACAATGTGAATGCGAGCA 399  
Db 248 GGGCAGCAGATCGGAGATGAGTCTTCTCCAGCAGTACAGCAACAATGTGAATGCGAGCA 307

QY 400 AAGAT 405  
Db 308 AAGAT 313

RESULT 15  
US-09-795-006A-54  
; Sequence 54, Application US/09795006A  
; Patent No. US20020151680A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo et al  
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR  
; FILE REFERENCE: 28967/35977B  
; CURRENT APPLICATION NUMBER: US/09/795,006A  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: US 60/205,331  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: US 60/185,205  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 54  
; LENGTH: 388  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Hybrid DNA  
; NAME/KEY: CDS  
; LOCATION: (8)..(385)  
US-09-795-006A-54

Query Match 54.8%; Score 233.4; DB 10; Length 388;  
Best Local Similarity 82.7%; Pred. No. 2.3e-62;  
Matches 267; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 100 GGGCAGATCATCAGCAAGTGGTGAAGTTCATGATGCTATCAGCGCAGCTACTGCCAT 159  
Db 8 GGGCAGATCATCAGCAAGTGGTGAAGTTCATGATGCTATCAGCGCAGCTACTGCCAT 67

QY 160 CCAATCGAGACCTGGTGGACATCTTCAGGAGTACCCTGATGAGATCGAGTACATCTTC 219  
Db 68 CCGATCGAGACCTGGTGGACATCTTCAGGAGTACCCTGATGAGATCGAGTACATCTTC 127

QY 220 AAGCCATCTGTGCCCTGTGATGCGGAGTCCCAACATCAGATTCGCGATCAACCTCACC 339  
Db 188 TCGTTCGCCAGGAGTCCCAACATCAGATTCGCGATCAACCTCACC 247

QY 340 GGGCAGCAGATAGGAGATGAGTCTTCTCCAGCAGTACAGCAACAATGTGAATGCGAGCA 399  
Db 248 GGGCAGCAGATCGGAGATGAGTCTTCTCCAGCAGTACAGCAACAATGTGAATGCGAGCA 307

QY 400 AAGATGAGCAAGCAAGAAA 422

Db 308 AAAGATTGGTCTTCGAACAAA 330  
||||| | |||||

Search completed: November 20, 2002, 03:30:41  
Job time : 248 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 20, 2002, 02:38:02 ; Search time 2195 Seconds  
(without alignments)  
3143.179 Million cell updates/sec

Title: US-09-884-050-1

Perfect score: 426

Sequence: 1 atgaactttctgtcttctg.....gagcaagacagaagtaa 426

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: gb\_gss:\*
- 18: em\_gss\_hum:\*
- 19: em\_gss\_inv:\*
- 20: em\_gss\_pln:\*
- 21: em\_gss\_vrt:\*
- 22: em\_gss\_fun:\*
- 23: em\_gss\_mam:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_other:\*
- 26: em\_gss\_pro:\*
- 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	402	94.4	528	14	B0674897
C 2	388.4	91.2	459	9	A1591060
C 3	325.2	76.3	752	14	B0780197
4	296	69.5	890	13	B1869727
5	270	63.4	600	12	BG803325
6	226.6	53.2	719	12	BG864739
					BG864739 602799154

C	7	204.4	48.0	534	14	BM991154	BM991154	UI-H-D10-
	8	203.2	47.7	649	12	BF679862	BF679862	602154448
	9	193.8	45.5	208	10	BE166230	BE166230	MR3-HT048
	10	185.8	43.6	600	12	BG802357	BG802357	0174-04 M
	11	147.4	34.6	540	9	AA308077	AA308077	EST178917
	12	145.4	34.1	953	14	BQ713895	BQ713895	AGENCOURT
C	13	139.4	32.7	618	13	BI295068	BI295068	UI-R-DK0-
	14	119.4	28.0	413	14	BM756993	BM756993	K-EST0035
	15	119.4	28.0	507	14	BM757090	BM757090	K-EST0035
	16	119.4	28.0	522	14	BM751763	BM751763	K-EST0028
	17	119.4	28.0	582	14	BM757101	BM757101	K-EST0035
	18	119.4	28.0	636	14	BM742573	BM742573	K-EST0015
	19	119.2	28.0	195	9	AU052024	AU052024	AU052024
	20	119	27.9	127	13	BI771285	BI771285	603054641
	21	119	27.9	963	14	BQ893335	BQ893335	AGENCOURT
	22	118.6	27.8	455	9	A1272466	A1272466	UK06G06.Y
	23	118.6	27.8	997	9	AL530856	AL530856	AL530856
	24	118.4	27.8	489	13	BI790853	BI790853	ld09h10.Y
	25	118.4	27.8	829	10	BE569697	BE569697	601331496
	26	118.4	27.8	933	14	BQ936933	BQ936933	AGENCOURT
	27	118.4	27.8	936	13	BI905649	BI905649	603167660
	28	118	27.7	890	14	BQ644755	BQ644755	AGENCOURT
	29	118	27.7	901	9	AL552106	AL552106	AL552106
	30	118	27.7	903	9	AL546005	AL546005	AL546005
	31	118	27.7	925	9	AL547463	AL547463	AL547463
	32	118	27.7	1023	9	AL543185	AL543185	AL543185
	33	118	27.7	1031	14	BQ070531	BQ070531	AGENCOURT
	34	117.6	27.6	869	9	AL552344	AL552344	AL552344
	35	117.6	27.6	963	9	AL540600	AL540600	AL540600
	36	117.4	27.6	759	13	BI685632	BI685632	603309146
	37	117.2	27.5	792	9	AL545800	AL545800	AL545800
	38	117.2	27.5	887	14	BQ881520	BQ881520	AGENCOURT
	39	117	27.5	1073	14	BQ070196	BQ070196	AGENCOURT
	40	116.8	27.4	744	13	BI663772	BI663772	603288511
	41	116.8	27.4	900	14	BQ647895	BQ647895	AGENCOURT
	42	116.4	27.3	488	14	HI11172	HI11172	ym09g08.r1
	43	116	27.2	590	13	BI345094	BI345094	373803 MA
	44	115.6	27.1	913	9	AL553367	AL553367	AL553367
	45	115.4	27.1	498	14	R19956	R19956	vg38b07.r1

#### ALIGNMENTS

RESULT 1  
B0674897  
LOCUS  
DEFINITION B0674897 AGNCOURT\_8036450 NIH\_MGC\_102 Homo sapiens cdna clone IMAGE:6212223  
5', mRNA sequence.  
ACCESSION B0674897  
VERSION B0674897.1 GI:21785731  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 528)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1CM2375 row: p column: 16  
High quality sequence stop: 527.  
Location/Qualifiers  
1. .528

linear EST 15-JUL-2002





ACCESSION BQ780197  
 VERSION BQ780197.1 GI:21988669  
 KEYWORDS EST.  
 SOURCE Rattus norvegicus  
 ORGANISM Norway rat.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 752)  
 Bernaldo, M.F., Lennon, G. and Soares, M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 97044477  
 Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 Tissue Procurement: Jeff Stevens  
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: DISTRIBUTION: Researchers may obtain clones  
 from Research Genetics (www.resgen.com).  
 The following repetitive elements were found in this CDNA  
 sequence: 1-39, >POLY(A)simple\_repeat (matched complement) 546-578;  
 >GC-rich#Low\_complexity (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES  
 source  
 Location/Qualifiers  
 1..752  
 /organism="Rattus norvegicus"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-PF0-cpb-1-06-0-UI"  
 /clone\_lib="UI-R-PF0"  
 /tissue.type="Mixed tissues"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /note="Vector: pT73-Pac (Pharmacia) with a modified  
 polylinker; Site 1: EcoR I; Site 2: Not I; UI-R-PF0 is a  
 subtracted CDNA library containing the following tissue(s)  
 ): Normal cartilage and SR-JWS Tumor Line . The  
 subtraction was made according to Bernaldo, Lennon and  
 Soares, Genome Research, 6:791-806, 1996. The  
 oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dT)18 tail. The  
 sequence tags for these libraries are: CTAATGGACG,  
 CATTCTTGTA.  
 TAG\_LIB=UI-R-PF0  
 TAG\_TISSUE=cartilage  
 TAG\_SEQ=CTAATGGACG"

BASE COUNT 109 a 246 c 205 g 189 t 3 others  
 ORIGIN  
 Query Match 76.3%; Score 325.2; DB 14; Length 752;  
 Best Local Similarity 86.9%; Pred. No. 4.9e-70;  
 Matches 370; Conservative 0; Mismatches 53; Indels 3; Gaps 1;  
 QY 1 ATGAACCTTCTGCTGTTGGGTGCATGGAGCCTTGCCCTGCTGCTACCTCCACCAT 60  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 431 ATGAACCTTCTGCTGTTGGGTGCATGGAGCCTTGCCCTGCTGCTACCTCCACCAT 372  
 QY 61 GCGAAGTGTCCAGGCTGCACCCATGGCAGAGAGGAGGCGGAGCAATCATCAGCAAGTG 120  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 371 GCGAAGTGTCCAGGCTGCACCCATGGCAGAGAGGAGGCGGAGCAATCATCAGCAAGTG 315  
 QY 121 GTGAAGTTCATGATGCTATACGCGAGCTACTGCCATCCAAATCGAGACCCCTGGTGGAC 180  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 314 GTGAAGTTCATGATGCTATACGCGAGCTACTGCCATCCAAATCGAGACCCCTGGTGGAC 255

QY 181 ATCTTCCAGGAGTACCTGATGAGATCGAGTACATCTTCAAGCCATCTCTGTGCCCTG 240  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 254 ATCTTCCAGGAGTACCTGATGAGATCGAGTACATCTTCAAGCCGCTCTGTGCCCTA 195  
 QY 241 ATGCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTGCCACTGAGGAGTCC 300  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 194 ATGCGGTGTGCGGGCTGCTGCAATGATGAAGCCCTGGAGTGTGTGCCACTGCGGAGC 135  
 QY 301 AACATCACCATGACAGATTATGCGGATCAACCTCACCAGGCCAGCACATAGGAGAGATG 360  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 134 AGCTCAGTATGAGATCATGCGGATCAACCTCACCAGGCCAGCACATAGGAGAGATG 75  
 QY 361 AGCTTCTACAGCACACAAATGTGAATGCAGACCAACAAAGAAAGATAGCAAGCAAGAA 420  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 74 AGCTTCTGCAGCATAGCAGATGTGAATGCAGACCAACAAAGAAAGATAGCAAGCAAGAA 15  
 QY 421 AAGTAA 426  
 || ||  
 Db 14 AAAAAA 9

RESULT 4  
 BI869727  
 LOCUS 603393614F1 NIH\_MGC\_90 Homo sapiens cDNA clone IMAGE:5403771 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI869727  
 VERSION BI869727.1 GI:16043400  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 890)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM12029 row: k column: 04  
 High quality sequence stop: 733.

FEATURES  
 source  
 Location/Qualifiers  
 1..890  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5403771"  
 /clone\_lib="NIH\_MGC\_90"  
 /tissue.type="adenocarcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: liver; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 1.7 Kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

BASE COUNT 246 a 246 c 256 g 142 t  
 ORIGIN  
 Query Match 69.5%; Score 296; DB 13; Length 890;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-63;  
 Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 127 TTCATGATGCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCCCTGGTGGACATCTTC 186  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 1 TTCATGATGCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCCCTGGTGGACATCTTC 60

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QY 187 CAGAGTACCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCCCTGATCGGA 246
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Db 61 CAGAGTACCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCCCTGATCGGA 120
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QY 247 TGGGGGGCTGCTGCAATGACGAGGGCTGAGTGTGTGCCCACTGAGGAGTCCACATC 306
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Db 121 TGGGGGGCTGCTGCAATGACGAGGGCTGAGTGTGTGCCCACTGAGGAGTCCACATC 180
|||||
QY 307 ACCATGCGAGATTATGCGGATCAAACTCCACCAAGGCCAGCACATAGGAGAGTGGAGTTC 366
|||||
Db 181 ACCATGCGAGATTATGCGGATCAAACTCCACCAAGGCCAGCACATAGGAGAGTGGAGTTC 240
|||||
QY 367 CTACAGCACAAATGTGAATGACAGACCAAGAAAGAGATAGACAGACAGAAAA 422
|||||
Db 241 CTACAGCACAAATGTGAATGACAGACCAAGAAAGAGATAGACAGACAGAAAA 296
|||||

RESULT 5
BG803325 600 bp mRNA linear EST 20-DEC-2001
LOCUS 0223-76 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
DEFINITION mRNA sequence.
ACCESSION BG803325
VERSION BG803325.1 GI:17950226
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Mu,X., Zhao, S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,
White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
21671825
Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.

FEATURES
Source
Location/Qualifiers
1..600
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/note="Vector: pAMP10 (Gibco); Cloned unidirectionally.
Primer: Oligo dt. RNA Isolation: cytoplasmic RNA preps
(Manniatlas); Cloning Technique: CUA Cloning (CloneAmp,
Life Technologies); Average insert size: 1.8 Kb;
Insertion site: TACGTCCTCAATCTGAGTG---. Other
information regarding entire library may be found at
http://pga.swmed.edu/Data/Libraries/microarray_cdna_librar
ies.htm."
BASE COUNT 131 a 183 c 196 g 90 t
ORIGIN
Query Match 63.4%; Score 270; DB 12; Length 600;
Best Local Similarity 86.6%; Pred. No. 2e-56;
Matches 310; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

QY 1 ATGAACCTTTCTGCTGCTTGGGTGCATTTGAGCCTTGCCTGCTCTACCTCCACCAT 60
|||||
Db 246 ATGAACCTTTCTGCTGCTTGGGTGCATTTGAGCCTTGCCTGCTCTACCTCCACCAT 305
|||||
QY 61 GCCAAGTGTCTCCAGGCTGCAGCCATCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
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Db 306 GCCAAGTGTCTCCAGGCTGCAGCCATCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 362
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QY 121 GTGAAGTTATGATGCTTATCATCGCCAGCTACTGCGCATCCATCCATCGAGAGCCCTGGTGGAC 180
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```

Db 363 ATCAAGTTCTATGATGTCTACCGAGAGCTACTGCGCTCCGATTGAGACCCCTGGTGGAC 422
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QY 181 ATCTTCAGGAGTACCTCTGATGAGTACGAGTACATCTTCAAGCCATCCTGTGTGCCCTG 240
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Db 423 ATCTTCAGGAGTACCCCGACGAGATAGATACATCTTCAAGCCGCTCTGTGTGCCCTG 482
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QY 241 ATCGATGCGGGGGCTGCTGCAATGACGAGGGCTGTGAGTGTGTGCCCACTGAGGAGTCC 300
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Db 483 ATCGCTGTGCGAGCTGCTGTAAAGATGAAGCCCTGGAGTGCCTGCCACGTCAGAGAGC 542
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QY 301 AACATCACCATGCGAGATTATGCGGATCAAACTCCACCAAGGCCAGCACATAGGAGAGA 358
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Db 543 AACATCACCATGCGAGATCATGCGGATCAAACTCCACCAAGGCCAGCACATAGGAGAGA 600
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RESULT 6
BG864739 719 bp mRNA linear EST 29-MAY-2001
LOCUS 602799154F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4934916 5',
DEFINITION mRNA sequence.
ACCESSION BG864739
VERSION BG864739.1 GI:14215277
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 719)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10864 row: k column: 13
High quality sequence stop: 715.

FEATURES
Source
Location/Qualifiers
1..719
/organism="Mus musculus"
/strain="NMRI"
/db_xref="taxon:10090"
/clone_lib="IMAGE:4934916"
/clone_lib="NCI_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies, Inc.
providing samples: Lothar Hennighausen/Priscilla Furth,
NIH Reference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
BASE COUNT 156 a 205 c 245 g 113 t
ORIGIN
Query Match 53.2%; Score 226.6; DB 12; Length 719;
Best Local Similarity 85.0%; Pred. No. 1.1e-45;
Matches 266; Conservative 0; Mismatches 44; Indels 3; Gaps 1;

QY 1 ATGAACCTTTCTGCTGCTTGGGTGCATTTGAGCCTTGCCTGCTCTACCTCCACCAT 60
|||||
Db 312 ATGAACCTTTCTGCTGCTTGGGTGCATTTGAGCCTTGCCTGCTCTACCTCCACCAT 371
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QY 61 GCCAAGTGTCTCCAGGCTGCAGCCATGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
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/clone="S6SNU620-22-C03"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F"
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/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
```

```
BASE COUNT      131 a  108 c  108 g  66 t
ORIGIN
```

```
Query Match      28.0%; Score 119.4; DB 14; Length 413;
Best Local Similarity 99.2%; Pred. No. 2.9e-19;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  304 ATCCATCGAGTATATGGGGATCAAACTCACCAGGCCAGCACATAGGAGATGAGC 363
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATCCATCGAGTATATGGGGATCAAACTCACCAGGCCAGCACATAGGAGATGAGC 60

QY  364 TTCCTACAGCACAAACAAATGTGAATGCAGACCAACCAAGATAGACCAAGAAAG 423
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TTCCTACAGCACAAACAAATGTGAATGCAGACCAACCAAGATAGACCAAGAAAG 120

QY  424 T 424
      |
Db   121 T 121
```

```
RESULT 15
BM757090
LOCUS      K-EST0035851 S6SNU620 Homo sapiens cDNA clone S6SNU620-21-D03 5',
DEFINITION mRNA sequence.
ACCESSION BM757090
VERSION    BM757090.1 GI:19086705
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 507)
AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
TITLE      21C Frontier Korean EST Project 2001
JOURNAL    Unpublished (2002)
COMMENT    Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel.: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 21 row: D column: 03
            High quality sequence stop: 507.
            Location/Qualifiers
FEATURES   source
            1..507
            /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="S6SNU620-21-D03"
/clone_lib="S6SNU620"
/sex="F"
/tissue_type="Ascites"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F"
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```
/note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
```

```
BASE COUNT      158 a  131 c  124 g  94 t
ORIGIN

Query Match      28.0%; Score 119.4; DB 14; Length 507;
Best Local Similarity 99.2%; Pred. No. 3e-19;
Matches 120; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  304 ATCCATCGAGTATATGGGGATCAAACTCACCAGGCCAGCACATAGGAGATGAGC 363
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATCCATCGAGTATATGGGGATCAAACTCACCAGGCCAGCACATAGGAGATGAGC 60

QY  364 TTCCTACAGCACAAACAAATGTGAATGCAGACCAACCAAGATAGACCAAGAAAG 423
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TTCCTACAGCACAAACAAATGTGAATGCAGACCAACCAAGATAGACCAAGAAAG 120

QY  424 T 424
      |
Db   121 T 121
```

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Search completed: November 20, 2002, 04:53:37
Job time : 2225 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 03:27:51 ; Search time 73 seconds  
(without alignments)  
257.374 Million cell updates/sec

Title: US-09-884-050-2

Perfect score: 792

Sequence: 1 MNFLSWHWSLALLYLHH.....FLQHNKCECRPKKDRARQEK 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	792	100.0	147	16 AAR91075	Human vascular end
2	792	100.0	147	17 AAR94001	VEGF121. Homo sap
3	792	100.0	147	19 AAW62524	Amino acid sequenc
4	792	100.0	147	21 AAY90402	VEGF encoded by cl
5	792	100.0	147	21 AAY69412	Amino acid sequenc
6	792	100.0	147	21 AAY83033	Human vascular end
7	792	100.0	147	22 AAB98080	Human VEGF splice
8	792	100.0	147	22 AAB50427	Human vascular end
9	792	100.0	147	22 AAB50431	Human VEGF121. Ho
10	792	100.0	147	23 ABB76299	Human vascular end

11	792	100.0	164	20 AAY43482	Amino acid sequenc
12	792	100.0	171	20 AAY07473	Human VEGF(145) pr
13	792	100.0	188	20 AAY43484	Amino acid sequenc
14	792	100.0	191	19 AAW62525	Amino acid sequenc
15	792	100.0	208	20 AAY43483	Amino acid sequenc
16	792	100.0	213	21 AAY83036	Human vascular end
17	792	100.0	213	22 AAB50434	Human VEGF189. Ho
18	792	100.0	213	23 ABB76302	Human vascular end
19	792	100.0	215	11 AAR05102	Human vascular per
20	792	100.0	215	16 AAR91077	Human vascular end
21	792	100.0	215	17 AAR94003	VEGF189. Homo sap
22	792	100.0	215	19 AAB62526	Amino acid sequenc
23	792	100.0	215	21 AAB10645	Human VEGF protein
24	792	100.0	215	21 AAY90404	VEGF encoded by cl
25	792	100.0	215	21 AAY69415	Amino acid sequenc
26	792	100.0	215	21 AAY94803	Human VEGF. Homo
27	792	100.0	215	21 AAY57035	Human A215 amino a
28	792	100.0	215	22 AAB37512	Human VEGF C subun
29	792	100.0	232	16 AAR91078	Human vascular end
30	792	100.0	232	17 AAR94004	VEGF206. Homo sap
31	792	100.0	232	19 AAW62527	Amino acid sequenc
32	792	100.0	232	20 AAY43481	Amino acid sequenc
33	792	100.0	232	21 AAY90405	VEGF encoded by cl
34	792	100.0	232	21 AAY69416	Amino acid sequenc
35	792	100.0	232	21 AAY83037	Human vascular end
36	792	100.0	232	22 AAU08464	Polypeptide for hu
37	792	100.0	232	22 AAB50435	Human VEGF206. Ho
38	792	100.0	232	23 ABB76303	Human vascular end
39	792	100.0	398	20 AAY29418	Human vascular end
40	787	99.4	174	22 AAB82531	Vascular endotheli
41	787	99.4	191	11 AAR08002	Human vascular end
42	787	99.4	191	16 AAR91076	Human vascular end
43	787	99.4	191	17 AAW00724	Vascular endotheli
44	787	99.4	191	17 AAR94002	VEGF165. Homo sap
45	787	99.4	191	19 AAB93331	Human VEGF protein

ALIGNMENTS

RESULT 1

AAR91075

ID AAR91075 standard; Protein; 147 AA.

XX AAR91075;

AC AAR91075;

XX 14-MAY-1996 (first entry)

XX Human vascular endothelial growth factor-121, VEGF-121.

DE Conjugate; growth factor; FGF; cytotoxin; saporin; eye; regulation;  
KW cell proliferation; psoriasis; pterygia; corneal clouding; cancer;  
KW rheumatoid arthritis; vascular endothelial; fibroblast; epidermal;  
KW heparin binding.  
KW Homo sapiens.  
OS Homo sapiens.  
PH Key Location/Qualifiers  
FT Peptide 1..26  
FT Protein /label= sig\_peptide  
FT 27..147  
FT /label= VEGF-121

XX WO9524928-A2.

XX 21-SEP-1995.

XX 15-MAR-1995; 95WO-US03448.

XX 15-MAR-1994; 94US-0213447.

XX 15-MAR-1994; 94US-0213446.

XX (PRIZ-) PRIZM PHARM INC.

XX PI Baird JA, Houston LL, Nova MP, Sosnowski BA;  
 XX WPI; 1995-336820/43.  
 XX DR N-PSDB; AAQ99080.  
 XX PI New conjugates of growth factor receptor ligand and targetted agent  
 PT - partic. DNA or cytotoxin, used to control cell proliferation in  
 PT the eye, e.g. to prevent growth of pterygii and corneal clouding  
 XX  
 XX PS Disclosure; Page 184-185; 204pp; English.  
 XX  
 CC AAR91075-R91078 are human vascular endothelial growth factors (VEGFs).  
 CC DNA encoding a VEGF can be used to create a fusion protein (FP),  
 CC the cDNA of which includes a nucleic acid binding domain (NABD) and  
 CC encodes a heparin binding growth factor, HEPGF (e.g. VEGF, HBEGF),  
 CC a protein synthesis inhibitor and opt. a linker imparting flexibility  
 CC to the FP. The FP can be used to target a protein synthesis inhibitor,  
 CC an antisense DNA sequence or an inhibitor of elongation factor 2, to a  
 CC cell carrying a HEPGF receptor. The conjugates of the invention are  
 CC used to inhibit cell proliferation in cells carrying the particular  
 CC growth factor receptor. A specific application is to prevent  
 CC excessive proliferation of epithelial cells, fibroblasts and  
 CC keratinocytes in the anterior eye after surgery, partic. to prevent  
 CC recurrence of pterygii after surgical removal, closure of  
 CC trabeculectomy after glaucoma surgery and corneal clouding after  
 CC exclamer laser treatment. Other conditions which may be treated include  
 CC tumours, restenosis, psoriasis, Dupuytren's contracture, diabetic  
 CC complications, Kaposi's sarcoma and rheumatoid arthritis.  
 XX  
 XX SQ Sequence 147 AA;  
 Query Match 100.0%; Score 792; DB 16; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-76;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVFMDVYQSYCHPIETLVD 60  
 QY 61 IFQEYPDEIEYIFKPSVPLMRCGGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 Db 61 IFQEYPDEIEYIFKPSVPLMRCGGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 QY 121 SFLQHNKCECRPKDRARQEK 141  
 Db 121 SFLQHNKCECRPKDRARQEK 141  
 RESULT 2  
 AAR94001  
 ID AAR94001 standard; Protein; 147 AA.  
 XX  
 AC AAR94001;  
 XX  
 DT 09-OCT-1996 (first entry)  
 XX  
 DE VEGF121.  
 XX  
 KW Vascular endothelial growth factor; VEGF; human; conjugate; tumour; iris;  
 KW proliferation inhibition; VEGF-mediated pathophysiological condition;  
 KW dermatological disorder; VEGF receptor; vascular proliferation; retina;  
 KW ophthalmic disorder; hyperproliferating blood vessel; therapy; psoriasis;  
 KW conjunctiva; vitreous humour; rheumatoid arthritis; skin cancer;  
 KW varicose veins; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX WO9606641-A1.  
 PN  
 XX  
 PD 07-MAR-1996.  
 XX  
 PF 29-AUG-1995; 95WO-US10973.

XX PR 16-MAY-1995; 95US-0441979.  
 XX PR 29-AUG-1994; 94US-0297961.  
 XX PA (PRIZ-) PRIZM PHARM INC.  
 XX PI Fleurbaaij GA, Freund E, Houston LL, Nova MP, Sosnowski BA;  
 PI Victor KD;  
 XX WPI; 1996-160151/16.  
 XX DR N-PSDB; AAT17613.  
 XX Vascular endothelial cell growth factor (VEGF) conjugates - having  
 PT VEGF linked to targeted agent, used for inhibiting proliferation of  
 PT cells, e.g. for gene therapy  
 XX  
 XX PS Disclosure; Page 122-123; 193pp; English.  
 XX  
 CC AAR94001-R94004, AAR94031, AAR94032, AAR94039 and AAR94040 represent  
 CC vascular endothelial growth factors (VEGF). This sequence represents  
 CC VEGF121. These sequences were used in VEGF conjugates of the invention.  
 CC In the conjugates, VEGF (or fragments of it) are linked to a targeted  
 CC agent (this can be via a linker sequence), so that the conjugate binds to  
 CC a VEGF receptor. Cys-modified forms of VEGF are particularly suitable  
 CC for chemical conjugation to linkers and targeted agents. The conjugates  
 CC are used for inhibiting proliferation of cells bearing VEGF receptors.  
 CC They can be used for treating a VEGF-mediated pathophysiological  
 CC condition, including dermatological disorders with underlying vascular  
 CC proliferation, solid tumours or an ophthalmic disorder of  
 CC hyperproliferating blood vessels of the retina, iris, conjunctiva or  
 CC vitreous humour. The conjugates can also be used for treating  
 CC psoriasis, rheumatoid arthritis, skin cancers and other tumours, or  
 CC varicose veins. They are also suitable for use in gene therapy.  
 XX  
 XX SQ Sequence 147 AA;  
 Query Match 100.0%; Score 792; DB 17; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-76;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVFMDVYQSYCHPIETLVD 60  
 QY 61 IFQEYPDEIEYIFKPSVPLMRCGGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 Db 61 IFQEYPDEIEYIFKPSVPLMRCGGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 QY 121 SFLQHNKCECRPKDRARQEK 141  
 Db 121 SFLQHNKCECRPKDRARQEK 141  
 RESULT 3  
 AAW62524  
 ID AAW62524 standard; Protein; 147 AA.  
 XX  
 AC AAW62524;  
 XX  
 DT 11-SEP-1998 (first entry)  
 XX  
 DE Amino acid sequence of human VEGF-121.  
 XX  
 KW Human; vascular endothelial growth factor; VEGF; production;  
 KW nitric oxide; prostacyclin; treatment; prevention; intimal hyperplasia;  
 KW blood vessel; essential hypertension; pulmonary arterial hypertension;  
 KW PAH; cor pulmonale; atherosclerosis; (re)stenosis; angioplasty;  
 KW coronary bypass operation; anastomosis; endarterectomy.  
 XX  
 OS Homo sapiens.  
 XX WO9820027-A2.  
 PN  
 XX

```

PD 14-MAY-1998.
XX
PF 03-NOV-1997; 97WO-GB03015.
XX
PR 21-AUG-1997; 97GB-0017791.
XX
PR 01-NOV-1996; 96GB-0022852.
XX
PR 09-MAY-1997; 97GB-0009494.
XX
FA (EURO-) EUROGENE LTD.
XX
XX Barker SGE, Martin JF, Yla-Herttuala S;
PI WPI; 1998-286857/25.
XX
DR N-PSDB; AAV38450.
XX
XX Treatment of prevention of intimal hyperplasia by stimulating
PT production of nitric oxide - by administration of vascular
PT endothelial growth factor, useful for, e.g. treating or preventing
PT intimal hyperplasia
XX
XX Claim 8; Page 54; 70pp; English.
XX
XX The present sequence represents human vascular endothelial growth factor
CC 121 (VEGF-121). VEGF stimulates production of nitric oxide and
CC prostacyclin. VEGF can therefore be used for treatment or prevention
CC of intimal hyperplasia in a blood vessel. VEGF can be used for treating
CC or preventing any condition responsive to in vivo stimulation of
CC nitric acid and prostacyclin (especially essential hypertension,
CC pulmonary arterial hypertension (PAH), cor pulmonale and
CC atherosclerosis. VEGF is specifically used to control (re)stenosis,
CC where caused by PAH or by a surgical procedure such as angioplasty,
CC coronary bypass operation, anastomosis or endarterectomy.
XX
XX Sequence 147 AA;
XX
Query Match 100.0%; Score 792; DB 19; Length 147;
Best Local Similarity 100.0%; Pred. No. 8.4e-76;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNFLLSVHWSLALLLLYHAKWSQAAPMAEGGGQNHHEVVKFMDVYORSYCHPIETLVD 60
Db 1 MNFLLSVHWSLALLLLYHAKWSQAAPMAEGGGQNHHEVVKFMDVYORSYCHPIETLVD 60
Qy 61 IFQEYPDEIEYIFKPSVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHQGHIGEM 120
Db 61 IFQEYPDEIEYIFKPSVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHQGHIGEM 120
Qy 121 SFLQHNKCECRPKDRARQEK 141
Db 121 SFLQHNKCECRPKDRARQEK 141
XX
RESULT 4
AAAY90402
ID AAAY90402 standard; Protein; 147 AA.
XX
AC AAAY90402;
XX
XX 18-JUL-2000 (first entry)
XX
DE VEGF encoded by clone VEGF121, SEQ ID NO:1.
XX
KW Targetted gene delivery; fibroblast growth factor receptor;
KW FGFR-binding protein; nucleic acid binding protein;
KW receptor-internalised ligand; cytotoxin; saporin; gene therapy;
KW cytotide; antiproliferative; cancer; melanoma; diabetic retinopathy;
KW rheumatoid arthritis; restenosis, Dupuytren's contracture; psoriasis;
KW eczema; heparin-binding epidermal growth factor; HBEGF;
KW vascular endothelial growth factor; VEGF.
XX
OS Unidentified.
XX
PN US6037329-A.

```

---

```

XX 14-MAR-2000.
XX
XX 24-SEP-1996; 96US-0718904.
XX
XX 15-MAR-1994; 94US-0213446.
XX
XX 15-MAR-1994; 94US-0213447.
XX
XX 29-AUG-1994; 94US-0297961.
XX
XX 13-SEP-1994; 94US-0305771.
XX
XX 16-MAY-1995; 95US-0441979.
XX
XX (SELE-) SELECTIVE GENETICS INC.
XX
XX Chandler LA, Sosnowski BA, Baird JA;
XX
XX WPI: 2000-292008/25.
XX
XX N-PSDB; AAA12853.
XX
XX Gene delivery system, useful for treating or preventing cancer and
PT rheumatoid arthritis, comprises receptor-internalized ligand linked to
PT nucleic acid binding domain and nucleic acid
XX
XX Disclosure; Columns 83-84; 131pp; English.
XX
XX The invention relates to a novel gene delivery composition for the
CC targetted delivery of cytotoxins or prodrug-converting enzymes to
CC proliferating cells. The gene delivery composition comprises a protein
CC that binds the fibroblast growth factor receptor (FGFR) which is fused
CC or chemically conjugated to a nucleic acid binding domain. The nucleic
CC acid binding domain is complexed with a suitable expression construct
CC encoding a cytotoxin such as saporin. One or more linkers may join the
CC FGFR-binding protein to the nucleic acid binding protein. These are
CC selected to increase the specificity, toxicity, solubility, serum
CC stability or intracellular availability, and may serve to promote
CC condensation of nucleic acids for delivery to a cell. The fusion protein
CC binds to FGFR and is internalised by cells that carry this receptor. The
CC gene delivery composition is used for the therapeutic alteration of the
CC function, gene expression and viability of cells. In particular, it may
CC be used for the treatment and prevention of cell proliferative
CC disorders, for example after eye surgery, melanoma and many other sorts
CC of cancer, rheumatoid arthritis, restenosis, Dupuytren's contracture,
CC diabetic retinopathy, psoriasis and eczema. The gene delivery
CC compositions of the invention have high specificity for particular cells
CC and can deliver larger amounts of DNA compared to prior art methods.
CC Sequences AAA12853- AAA12856 represent cDNA clones encoding vascular
CC endothelial growth factor (VEGF), and sequences XAY90402-Y90405 represent
CC the encoded VEGF proteins. AAA12857 represents cDNA encoding human
CC heparin-binding epidermal growth factor (HBEGF) precursor, and
CC XAY90406-Y90409 represent HBEGF precursor and mature proteins.
XX
XX Sequence 147 AA;
XX
Query Match 100.0%; Score 792; DB 21; Length 147;
Best Local Similarity 100.0%; Pred. No. 8.4e-76;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MNFLLSVHWSLALLLLYHAKWSQAAPMAEGGGQNHHEVVKFMDVYORSYCHPIETLVD 60
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Db 61 IFQEYPDEIEYIFKPSVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHQGHIGEM 120
Qy 121 SFLQHNKCECRPKDRARQEK 141
Db 121 SFLQHNKCECRPKDRARQEK 141
XX
RESULT 5
AAAY9412
ID AAAY69412 standard; Protein; 147 AA.
XX

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AC AAY69412;  
 XX  
 DT 03-JUL-2000 (first entry)  
 XX  
 DE Amino acid sequence of vascular endothelial growth factor 121.  
 XX  
 KW Human; vascular endothelial growth factor; VEGF 121; angiogenic factor;  
 KW blood vessel injury; vascular injury; microvascular angiopathy;  
 KW thrombotic microangiopathy; kidney disease; haemolytic uremic syndrome;  
 KW toxic shock syndrome; venom; hypercoagulable state; platelet activation;  
 KW platelet aggregation; thrombosis; preclampsia; sepsis; pancreatitis;  
 KW intravascular coagulation; thrombotic thrombocytopenia purpura;  
 KW acute renal failure; myocardial infarction; ischemic bowel disease;  
 KW stroke; hypoxia; hypercapnia; fibrosis; toxic alveolar injury;  
 KW acute respiratory distress syndrome; pneumonia; pulmonary emboli;  
 KW birth prematurity disorder; wound; allergy; hypersensitivity;  
 KW autoimmune disease; organ transplant; focal glomerulosclerosis;  
 KW amyloidosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200013702-A2.  
 XX  
 PD 16-MAR-2000.  
 XX  
 PF 09-SEP-1999; 99WO-US20480.  
 XX  
 PR 09-SEP-1998; 98US-0099694.  
 PR 26-MAR-1999; 99US-0126406.  
 PR 27-MAR-1999; 99US-0126615.  
 XX  
 PA (SCIO-) SCIOS INC.  
 XX  
 PI Schreiner GF, Johnson RJ;  
 XX  
 DR WPI: 2000-256861/22.  
 DR N-PSDB; AA299344.  
 XX  
 PT Novel methods and compositions for the prevention and treatment of  
 PT microvascular angiopathies by administration of angiogenic factors such  
 PT as vascular endothelial growth factor (VEGF)  
 XX  
 PS Disclosure; Fig 3; 46pp; English.  
 XX  
 CC The present sequence represents native human vascular endothelial growth  
 CC factor (VEGF) 121. VEGF is an angiogenic factor. VEGF proteins are used  
 CC for the prevention or repair of injury to blood vessels or associated  
 CC nonvascular tissues (served by the blood vessels) and for the prevention  
 CC and repair of vascular injury associated with microvascular angiopathy,  
 CC particularly thrombotic microangiopathy. The proteins methods may also  
 CC be used for the prevention and treatment of kidney diseases associated  
 CC with injury to, or atrophy of, the vasculature of the glomerulus and  
 CC interstitium. Conditions which may be treated include haemolytic uremic  
 CC syndrome, toxic shock syndrome, venom exposure, chemical exposure,  
 CC hypercoagulable states, platelet activation or aggregation, thrombosis,  
 CC preclampsia, thrombotic thrombocytopenia purpura, disseminated  
 CC intravascular coagulation, sepsis, pancreatitis, acute renal failure,  
 CC myocardial infarction, ischemic bowel disease, transient ischemic  
 CC attacks, stroke, hypoxia or hypercapnia or fibrosis arising from lung  
 CC endothelium injury, acute respiratory distress syndrome, toxic alveolar  
 CC injury, pneumonia, pulmonary emboli, birth prematurity disorders,  
 CC wounds, allergic reactions, hypersensitivity, autoimmune diseases, organ  
 CC transplants, focal glomerulosclerosis, and amyloidosis.  
 XX  
 SQ Sequence 147 AA;  
 Query Match 100.0%; Score 792; DB 21; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-76;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNFLSWHNSALLLYLHAKWSQAAPMAEGGQNHHEVVKFMDYQRSYCHPIETLYD 60  
 DB 1 MNFLSWHNSALLLYLHAKWSQAAPMAEGGQNHHEVVKFMDYQRSYCHPIETLYD 60

QY 61 IFQEXPDEIEYIFKPSVPLMRGCGCCNDGECVPTESNITMQIMRIKPHOGHIGEM 120  
 DB 61 IFQEXPDEIEYIFKPSVPLMRGCGCCNDGECVPTESNITMQIMRIKPHOGHIGEM 120  
 QY 121 SFLQHNKCECRPKKORAROEK 141  
 DB 121 SFLQHNKCECRPKKORAROEK 141  
 RESULT 6  
 ID AAY83033 standard; Protein; 147 AA.  
 AC AAY83033;  
 XX 04-JUL-2000 (first entry)  
 XX  
 DE Human vascular endothelial growth factor (hVEGF121).  
 XX  
 KW Vascular endothelial growth factor; human; angiogenesis; VEGF;  
 KW capillary formation; hypertension; treatment; kidney; CNS; stroke;  
 KW meningitis; central nervous system; tumour; infection; bone growth;  
 KW hypoxia; hypercapnia; fibrosis; inflammatory bowel disease;  
 KW diarrhoea; allografts; cardiac valve.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200013703-A2.  
 XX  
 PD 16-MAR-2000.  
 XX  
 PF 09-SEP-1999; 99WO-US20481.  
 XX  
 PR 09-SEP-1998; 98US-0099694.  
 PR 26-MAR-1999; 99US-0126406.  
 PR 27-MAR-1999; 99US-0126615.  
 XX  
 PA (SCIO-) SCIOS INC.  
 XX  
 PI Schreiner GF, Johnson RJ;  
 XX  
 DR WPI: 2000-256862/22.  
 DR N-PSDB; AA293345.  
 XX  
 PT Novel methods for treating hypertension by administering a factor which  
 PT increases angiogenesis and/or vascular permeability  
 XX  
 PS Claim 5; Figure 6; 51pp; English.  
 CC Administering vascular endothelial growth factor (VEGF) can be used  
 CC for treating hypertension (especially salt-dependent hypertension)  
 CC Administration of VEGF promotes angiogenesis and/or vascular or  
 CC capillary permeability. The method is also useful in treating  
 CC disorders related to abnormal transport of solutes across endothelial  
 CC cells. Such disorders include the treatment or prevention of kidney  
 CC disease associated with impaired filtration or excretion of solutes;  
 CC the treatment or prevention of diseases of the central nervous system  
 CC associated with alterations in cerebrospinal fluid, e.g. stroke,  
 CC meningitis, tumour, infections, and bone growth disorders; treatment  
 CC or prevention of hypoxia or hypercapnia or fibrosis arising from  
 CC accumulation of fluid secretions in the lungs, e.g. acute respiratory  
 CC distress syndrome, toxic alveolar injury, pneumonia, infections,  
 CC surgical intervention, cystic fibrosis; treatment or prevention of  
 CC pulmonary dysfunction arising from injury to the pulmonary  
 CC endothelium, including disorders arising from premature birth, and  
 CC pulmonary hypertension; treatment or prevention of disease arising  
 CC from disordered transport of fluid and solutes across the intestinal  
 CC epithelium, e.g. inflammatory bowel disease, diarrhoea; treatment or  
 CC prevention of ascites accumulation in the peritoneum; enhancement of  
 CC efficacy of solute flux; preservation or enhancement of function of  
 CC organ allografts; and treatment of cardiac valve disease. This  
 CC sequence is the native human vascular endothelial growth

CC factor hVEGF121. The activity of VEGF is mediated by interaction  
 CC with specific receptors on target tissues, most notably the vascular  
 CC endothelium. VEGF exists as five different length monomer chains due  
 CC to alternative splicing of the VEGF RNA transcript. VEGF121 is  
 CC unique among the five forms in that it does not bind to heparin like  
 CC molecules associated with the extracellular matrix.

XX SQ Sequence 147 AA;  
 Query Match 100.0%; Score 792; DB 21; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-76;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 Db 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 Qy 61 IFQEPDIEIYIFKPCVPLMRGCGCCNDGEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 Db 61 IFQEPDIEIYIFKPCVPLMRGCGCCNDGEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 Qy 121 SFLQHNKCECRPKKDRARQEK 141  
 Db 121 SFLQHNKCECRPKKDRARQEK 141

RESULT 7  
 AAB98080  
 ID AAB98080 standard; Protein; 147 AA.  
 XX AC AAB98080;  
 XX DT 16-AUG-2001 (first entry)  
 XX DE Human VEGF splice variant VEGF121 protein SEQ ID NO:4.  
 XX KW Human; vascular endothelial growth factor; VEGF splice variant; VEGF;  
 KW VEGF121; colon cancer cell line acquired malignancy; anticancer.

XX OS Homo sapiens.

FH Key Location/Qualifiers  
 FT Peptide 1..26  
 FT /label= signal  
 FT Protein 27..147  
 FT /label= VEGF\_splice\_variant\_VEGF121

XX JP2001061483-A.  
 XX PD 13-MAR-2001.  
 XX PF 31-AUG-1999; 95JP-0244198.  
 XX PR 31-AUG-1999; 95JP-0244198.  
 XX PA (EISA ) EISAI CO LTD.  
 XX WPI; 2001-294711/31.  
 XX N-PSDB; AAB21876.  
 XX Human colon cancer cell line is transfected with VEGF gene and selected  
 XX for having acquired malignancy -  
 XX Example 1; Page 7; 8pp; Japanese.

XX The present invention describes a method in which the vascular  
 CC endothelial growth cell (VEGF) gene is introduced to a human colon  
 CC cancer cell showing no malignancy, and a cell line highly expressing  
 CC VEGF is selected to get a cell line acquired malignancy. Also described  
 CC are: (1) a human colon cancer cell line acquired malignancy by the above  
 CC method; (2) WDR cell line acquired malignancy by the above method;  
 CC (3) a method for screening an anticancer agent by using the above human  
 CC colon cancer cell line, preferably WDR cell line, acquired malignancy;

CC and (4) a compound screened by the above method. The human colon cancer  
 CC cell line acquired malignancy can be used for screening an anticancer  
 CC agent. The present sequence represents the human VEGF splice variant  
 CC VEGF121, which is used in an example from the present invention.

XX SQ Sequence 147 AA;

Query Match 100.0%; Score 792; DB 22; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-76;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 Db 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 Qy 61 IFQEPDIEIYIFKPCVPLMRGCGCCNDGEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 Db 61 IFQEPDIEIYIFKPCVPLMRGCGCCNDGEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
 Qy 121 SFLQHNKCECRPKKDRARQEK 141  
 Db 121 SFLQHNKCECRPKKDRARQEK 141

RESULT 8  
 AAB50427  
 ID AAB50427 standard; Protein; 147 AA.

XX AC AAB50427;

XX DT 13-MAR-2001 (first entry)

XX DE Human vascular endothelial growth factor polypeptide.

XX KW Human; vascular endothelial growth factor; VEGF; VEGF dimer;  
 KW hypotensive; litholytic; nephrotropic; antiarteriosclerotic;  
 KW antiinflammatory; angiogenesis; vascular remodelling; injury; wound;  
 KW peripheral arterial disease; coronary artery disease; hypoxia;  
 KW essential hypertension; microvascular angiopathy; hypercapnia;  
 KW polycystic kidney disease; vascular endothelial cell repair;  
 KW lung disease; kidney disease; inflammatory bowel disease.

XX OS Homo sapiens.

XX WO200071716-A2.

XX PD 30-NOV-2000.

XX PF 18-MAY-2000; 2000WO-US13636.

XX PR 20-MAY-1999; 99US-0135312.

XX PR 20-JAN-2000; 2000US-0177407.

XX PA (SCIO-) SCIOS INC.

XX PI Jue RA, Schellenberger U, Stathis PA, Adriaenssens PI, Abraham JA;  
 PI Baldwin PA, Pollitt NS;

XX WPI; 2001-041064/05.

XX N-PSDB; AAC90473.

XX Vascular endothelial growth factor dimer, useful for treating essential  
 PT hypertension, polycystic kidney diseases, microvascular angiopathy and  
 PT coronary artery disease, comprising two monomeric subunits

XX Example 1; Fig 1; 61pp; English.

XX The present sequence encodes a monomer of a vascular endothelial growth  
 CC factor (VEGF) dimer. The dimer comprises a first and a second monomer,  
 CC each comprising at least amino acids 11-116 of a defined 147 amino acid  
 CC sequence, or a sequence having at least 90% identity to the defined  
 CC sequence, and retaining a cysteine at or corresponding to position 116,  
 CC which is disulphide-bonded to an additional extraneous cysteine. The

VEGF dimer is useful for inducing angiogenesis and vascular remodelling, treating peripheral arterial disease, coronary artery disease, essential hypertension, microvascular angiopathy and polycystic kidney disease, and repair of vascular endothelial cell layers. It is also useful for treating injuries, wounds, hypoxia, hypercapnia, pulmonary dysfunction, kidney diseases, diseases arising from disordered transport of solutes and fluids across the intestinal epithelium including inflammatory bowel disease, and disorders due to accumulation of ascites in the peritoneum.

Sequence 147 AA;

Query Match 100.0%; Score 792; DB 22; Length 147;

Best Local Similarity 100.0%; Pred. No. 8.4e-76;

Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLLSVHWSLALLLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60

DB 1 MNFLLSVHWSLALLLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60

QY 61 IFQEPDEIEYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRKPHOGQHIGEM 120

DB 61 IFQEPDEIEYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRKPHOGQHIGEM 120

QY 121 SFLQHNKCECRPKKDRARQEK 141

DB 121 SFLQHNKCECRPKKDRARQEK 141

RESULT 9

AAB50431

ID AAB50431 standard; Protein; 147 AA.

XX AAB50431;

XX 13-MAR-2001 (first entry)

DE Human VEGF121.

XX Human; VEGF; vascular endothelial growth factor; VEGF121; VEGF145;

KW cardiant; cerebroprotective; hypotensive; nephrotropic; antidiabetic;

KW dermatological; immunosuppressive; antiinflammatory; cytostatic;

KW vasotropic; antibacterial; angiogenesis; vascular remodelling;

KW vascular disease; kidney disease; diabetes; systemic lupus erythematosus;

KW meningitis; tumour; infection; lung disease inflammatory bowel disease.

XX Homo sapiens.

XX WO200071713-A1.

XX 30-NOV-2000.

XX 18-MAY-2000; 2000WO-US13536.

XX 20-MAY-1999; 99US-0135312.

XX (SCIO-) SCIOS INC.

XX Pollitt NS, Abraham JA;

XX WPI; 2001-025162/03.

XX N-PSDB; AAC90477.

XX Enhancing biological activity of vascular endothelial growth factor by

PT replacing a Cys residue, for producing variant useful for treating

PT hypertension, stroke, diabetes, lupus, glomerulonephritis, meningitis,

PT tumor, pneumonia, infections -

XX Claim 5; Fig 3; 62pp; English.

XX The present sequence is given in a specification relating to a method for

CC enhancing the biological activity of a vascular endothelial growth factor

CC (VEGF) originally having a cysteine residue at a position 116 of the 121

CC amino acid native mature human VEGF. The method comprises eliminating the  
CC cysteine residue to produce a VEGF variant. The variant is useful for  
CC inducing angiogenesis or vascular remodelling, for prevention or repair  
CC of injury to blood vessels, where injury is associated with haemolytic  
CC uraemic syndrome (HUS) or microvascular angiopathy such as thrombotic  
CC microangiopathy (TMA). The VEGF variant is also useful for treatment of  
CC essential hypertension in a patient. The variant is useful for treating  
CC coronary artery disease and/or peripheral arterial disease, to foster  
CC myocardial blood vessel growth and to improve blood flow to the heart. It  
CC is useful for the treatment and prevention of kidney diseases associated  
CC with injury to, or atrophy of, the vasculature of the glomerulus and  
CC interstitium and for the treatment and prevention of acute renal failure,  
CC myocardial infarction, ischaemic bowel disease, transient ischaemic  
CC attacks, stroke, hypoxia, hypercapnia, focal glomerulosclerosis,  
CC amyloidosis, glomerulonephritis, diabetes, systemic lupus erythematosus  
CC or chronic hypoxia/atrophy. It is also useful in the preservation or  
CC enhancement of function of organ allografts and xenografts, and for  
CC treating disorders related to abnormal transport of solutes across  
CC endothelial cells such as meningitis, tumour, infections, disorders of  
CC bone growth, acute respiratory distress syndrome, toxic alveolar injury,  
CC pneumonia, cystic fibrosis, inflammatory bowel disease, infectious  
CC diarrhoea or cardiac valve disease.

XX Sequence 147 AA;

Query Match 100.0%; Score 792; DB 22; Length 147;

Best Local Similarity 100.0%; Pred. No. 8.4e-76;

Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLLSVHWSLALLLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60

DB 1 MNFLLSVHWSLALLLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60

QY 61 IFQEPDEIEYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRKPHOGQHIGEM 120

DB 61 IFQEPDEIEYIFKPCVPLMRGCGCCNDGECVPTESNITMQIMRKPHOGQHIGEM 120

QY 121 SFLQHNKCECRPKKDRARQEK 141

DB 121 SFLQHNKCECRPKKDRARQEK 141

RESULT 10

ABB76299

ID ABB76299 standard; Protein; 147 AA.

XX ABB76299;

XX 12-AUG-2002 (first entry)

XX Human vascular endothelial growth factor 121.

XX Vascular endothelial growth factor; VEGF; hVEGF121; human;

KW hypertension; hypotensive; nephrotropic; cerebroprotective;

KW antibacterial; cytostatic; antialcoholic; virucide; vasotropic;

KW antiarrhythmic; immunosuppressive; cardiant; antiinflammatory;

KW angiogenic factor.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..26

FT /label= Signal\_peptide

FT Protein 27..147

FT /label= Mature\_protein

XX US6352975-B1.

XX 05-MAR-2002.

XX 09-SEP-1999; 99US-0392932.

XX 09-SEP-1998; 98US-099694P.

PR 26-MAR-1999; 99US-126406P.  
 PR 27-MAR-1999; 99US-126615P.  
 XX (SCIO-) SCIOS INC.  
 XX  
 XX Schreiner GF, Johnson RJ;  
 DR WPI; 2002-412951/44.  
 DR N-PSDB; ABL57427.  
 XX  
 XX New method, useful in treatment of salt-sensitive hypertension,  
 PT comprises administration of a vascular endothelial growth factor to a  
 PT patient -  
 XX  
 XX  
 PS Claim 1; Fig 6; 30pp; English.  
 XX  
 XX The present sequence is the protein sequence of human vascular  
 CC endothelial growth factor 121 (hVEGF121), an isoform that is weakly  
 CC acidic and does not bind to heparin. The present invention  
 CC concerns methods for the treatment of salt-sensitive hypertension  
 CC by administering a VEGF in an amount effective to reduce the blood  
 CC pressure of a salt-sensitive hypertension patient to a normal range.  
 CC The VEGF is preferably hVEGF121 or a VEGF having a heparin-binding  
 CC domain modified to render it incapable of binding heparin. The  
 CC VEGF may be co-administered with another angiogenic factor. The  
 CC method can also be used to treat disorders relating to abnormal  
 CC transport of solutes across endothelial cells, including treatment  
 CC or prevention of kidney disease associated with impaired filtration  
 CC or excretion of solutes, central nervous system diseases associated  
 CC with alterations in cerebrospinal fluid synthesis, composition or  
 CC circulation including stroke, meningitis, tumour, infections, and  
 CC disorders of bone growth, hypoxia or hypercapnia or fibrosis  
 CC arising from accumulation of fluid secretions in lungs or  
 CC impediments to their removal, including acute respiratory distress  
 CC syndrome, toxic alveolar injury as occurs in smoke inhalation,  
 CC pneumonia including viral and bacterial infections, surgical  
 CC interventions, cystic fibrosis, and other inherited or acquired  
 CC disease of the lung associated with fluid accumulation in the  
 CC pulmonary air space, pulmonary endothelium injury, disordered  
 CC transport of fluid and solutes across the intestinal epithelium,  
 CC including inflammatory bowel disease, infections, diarrhoea,  
 CC ascites accumulation in the peritoneum as occurs in the failure of  
 CC heart, liver and kidney, preservation and enhancement of function  
 CC of organ allografts, and cardiac valve disease.  
 XX Sequence 147 AA;  
 SQ  
 Query Match 100.0%; Score 792; DB 23; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-76;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNFLSWHWSLALLYLHAKWSQAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 DB 1 MNFLSWHWSLALLYLHAKWSQAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 QY 61 IFQEYPDEIEYIFKPCVPLMRGCGCNDGEGLECYPTESNITMQIMRKPHQGQHIGEM 120  
 DB 61 IFQEYPDEIEYIFKPCVPLMRGCGCNDGEGLECYPTESNITMQIMRKPHQGQHIGEM 120  
 QY 121 SFLQHNKCECRPKKDRARQEK 141  
 DB 121 SFLQHNKCECRPKKDRARQEK 141  
 RESULT 11  
 AAY43482  
 ID AAY43482 standard; Protein; 164 AA.  
 XX  
 AC AAY43482;  
 XX  
 DT 26-JAN-2000 (first entry)  
 XX  
 DE Amino acid sequence of VEGF-A138 protein.

XX Vascular endothelial factor; VEGF; VEGF-A138; variant; vascular disease;  
 KW cardiovascular disease; vascular cell proliferation; angioplasty;  
 KW restenosis; drug permeation; tumour; ischemic condition;  
 KW cardiac infarction; chronic coronary ischemia; stroke; wound treatment;  
 KW chronic lower limb ischemia; peripheral vascular disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT Peptide 1..27 "secretion signal sequence"  
 FT  
 XX  
 PN WO9940197-A2.  
 XX  
 PD 12-AUG-1999.  
 XX  
 XX 04-FEB-1999; 99WO-US02425.  
 PF  
 XX 06-FEB-1998; 98US-0073979.  
 PR  
 XX (COLL-) COLLATERAL THERAPEUTICS INC.  
 PA  
 XX Baird A, Andreason G;  
 PI WPI; 1999-600967/51.  
 DR N-PSDB; AAZ29996.  
 XX  
 XX New growth factor variants, useful for treating cardiovascular disease,  
 PT especially by stimulating vascular cell proliferation -  
 XX  
 XX Claim 7; Fig 3; 101pp; English.  
 XX  
 CC The present sequence represents vascular endothelial factor VEGF-A138.  
 CC It is a VEGF-A variant of the invention. The specification describes new  
 CC VEGF-A variants in which exon 6a is excluded (other forms which contain  
 CC both exon 6a and 6b are also described). The variants have a modified  
 CC affinity for matrix and low affinity receptors. This alters the  
 CC bioavailability of the proteins when administered directly to cells.  
 CC These variants are used to treat vascular disease, especially  
 CC cardiovascular disease, by stimulating vascular cell proliferation. They  
 CC enhance epithelialisation of diseased vessels, especially after  
 CC angioplasty. The re-endothelialisation reduces or prevents restenosis.  
 CC They are also useful for enhancing drug permeation by tumours and for  
 CC treating ischemic conditions such as cardiac infarction, chronic coronary  
 CC ischemia, chronic lower limb ischemia, stroke and peripheral vascular  
 CC disease. In addition they may be used to treat wounds.  
 XX  
 SQ Sequence 164 AA;  
 Query Match 100.0%; Score 792; DB 20; Length 164;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-76;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNFLSWHWSLALLYLHAKWSQAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 DB 1 MNFLSWHWSLALLYLHAKWSQAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 QY 61 IFQEYPDEIEYIFKPCVPLMRGCGCNDGEGLECYPTESNITMQIMRKPHQGQHIGEM 120  
 DB 61 IFQEYPDEIEYIFKPCVPLMRGCGCNDGEGLECYPTESNITMQIMRKPHQGQHIGEM 120  
 QY 121 SFLQHNKCECRPKKDRARQEK 141  
 DB 121 SFLQHNKCECRPKKDRARQEK 141  
 RESULT 12  
 AAY07473  
 ID AAY07473 standard; Protein; 171 AA.  
 XX  
 AC AAY07473;  
 XX

DT 03-AUG-1999 (first entry)  
 DE Human VEGF(145) protein sequence.  
 XX  
 KW Human;vascular endothelial growth factor; VEGF; vector; stimulation;  
 KW angiogenesis; mammal; peripheral; cardiac; tissue; ischaemia; perfusion;  
 KW neovascularisation; muscle.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..26  
 FT /note= "signal peptide"  
 FT Protein 27..171  
 FT /note= "mature protein"  
 XX  
 XX WO9921590-A1.  
 XX  
 XX 06-MAY-1999.  
 XX  
 XX 23-OCT-1998; 98WO-US22668.  
 XX  
 XX 26-NOV-1997; 97GB-0024906.  
 XX  
 XX 27-OCT-1997; 97US-0063629.  
 XX  
 XX (MERI ) MERCK & CO INC.  
 XX  
 XX Bett AJ, Huckie WR, Kendall RL, Thomas KA;  
 XX  
 XX WPI; 1999-302907/25.  
 XX  
 XX N-PSDB; AAX57724.  
 XX  
 XX Stimulating angiogenesis by expressing vascular endothelial growth  
 XX factor  
 XX  
 XX Example 1; Fig 2; 46pp; English.  
 XX  
 CC This sequence represents the 145 amino acid form of human vascular  
 CC endothelial growth factor (VEGF(145)). The coding sequence, when  
 CC administered in a vector, can be used to stimulate angiogenesis in a  
 CC mammal. Administration of the VEGF(145) is used to treat peripheral  
 CC cardiac or other tissue ischaemias, i.e. to increase neovascularisation,  
 CC perfusion and performance of ischaemic muscle.  
 XX  
 XX Sequence 171 AA;  
 SQ  
 Query Match 100.0%; Score 792; DB 20; Length 171;  
 Best Local Similarity 100.0%; Pred. No. 1e-75;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNFLLSVVHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 DB 1 MNFLLSVVHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 QY 61 IFQEYDPEIEYIFKPCVPLMRGCGCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120  
 DB 61 IFQEYDPEIEYIFKPCVPLMRGCGCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120  
 QY 121 SFLQHNKCECRPKKDRARQEK 141  
 DB 121 SFLQHNKCECRPKKDRARQEK 141  
 RESULT 13  
 AAY43484  
 ID AAY43484 standard; Protein; 188 AA.  
 XX  
 AC AAY43484;  
 XX  
 XX 26-JAN-2000 (first entry)  
 DT  
 XX Amino acid sequence of VEGF-A162 protein.  
 DE  
 XX

KW Vascular endothelial factor; VEGF; VEGF-A162; variant; vascular disease;  
 KW cardiovascular disease; vascular cell proliferation; angioplasty;  
 KW restenosis; drug permeation; tumour; ischemic condition;  
 KW cardiac infarction; chronic coronary ischemia; stroke; wound treatment;  
 KW chronic lower limb ischemia; peripheral vascular disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..27  
 FT /note= "secretion signal sequence"  
 XX  
 PN WO9940197-A2.  
 XX  
 XX 12-AUG-1999.  
 XX  
 XX 04-FEB-1999; 99WO-US02425.  
 XX  
 XX 06-FEB-1998; 98US-0073979.  
 XX  
 XX (COLL-) COLLATERAL THERAPEUTICS INC.  
 XX  
 XX Baird A, Andreason G;  
 XX  
 XX WPI; 1999-600967/51.  
 XX  
 XX N-PSDB; AA229998.  
 XX  
 XX New growth factor variants, useful for treating cardiovascular disease,  
 XX especially by stimulating vascular cell proliferation -  
 XX  
 XX Claim 9; Fig 5; 101pp; English.  
 CC  
 CC The present sequence represents vascular endothelial factor VEGF-A162.  
 CC It is a VEGF-A variant of the invention. The specification describes new  
 CC VEGF-A variants in which exon 6a is excluded (other forms which contain  
 CC both exon 6a and 6b are also described). The variants have a modified  
 CC affinity for matrix and low affinity receptors. This alters the  
 CC bioavailability of the proteins when administered directly to cells.  
 CC These variants are used to treat vascular disease, especially  
 CC cardiovascular disease, by stimulating vascular cell proliferation. They  
 CC enhance epithelialisation of diseased vessels, especially after  
 CC angioplasty. The re-endothelialisation reduces or prevents restenosis.  
 CC They are also useful for enhancing drug permeation by tumours and for  
 CC treating ischemic conditions such as cardiac infarction, chronic coronary  
 CC ischemia, chronic lower limb ischemia, stroke and peripheral vascular  
 CC disease. In addition they may be used to treat wounds.  
 XX  
 XX Sequence 188 AA;  
 SQ  
 Query Match 100.0%; Score 792; DB 20; Length 188;  
 Best Local Similarity 100.0%; Pred. No. 1.e-75;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNFLLSVVHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 DB 1 MNFLLSVVHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
 QY 61 IFQEYDPEIEYIFKPCVPLMRGCGCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120  
 DB 61 IFQEYDPEIEYIFKPCVPLMRGCGCNDGECVPTESNITMQIMRIKPHOGQHIGEM 120  
 QY 121 SFLQHNKCECRPKKDRARQEK 141  
 DB 121 SFLQHNKCECRPKKDRARQEK 141  
 RESULT 14  
 AAW62525  
 ID AAW62525 standard; Protein; 191 AA.  
 XX  
 XX AAW62525;  
 AC  
 XX 11-SEP-1998 (first entry)  
 DT



XX DE Amino acid sequence of human VEGF-165.  
XX KW Human; vascular endothelial growth factor; VEGF; production;  
XX KW nitric oxide; prostacyclin; treatment; prevention; intimal hyperplasia;  
XX KW blood vessel; essential hypertension; pulmonary arterial hypertension;  
XX KW PAH; cor pulmonale; atherosclerosis; (re)stenosis; angioplasty;  
XX KW coronary bypass operation; anastomosis; endarterectomy.  
XX OS Homo sapiens.  
XX XX  
XX PN WO9820027-A2.  
XX FT 14-MAY-1998.  
XX PD  
XX PF 03-NOV-1997; 97WO-GB03015.  
XX XX  
XX PR 21-AUG-1997; 97GB-0017791.  
XX PR 01-NOV-1996; 96GB-0022852.  
XX PR 09-MAY-1997; 97GB-0009494.  
XX XX  
XX PA (EURO-) EUROGENE LTD.  
XX XX  
XX PI Barker SGE, Martin JF, Yla-Herttuala S;  
XX XX  
XX DR WPI; 1998-286857/25.  
XX DR N-PSDB; AAV38451.  
XX XX  
XX PT Treatment or prevention of intimal hyperplasia by stimulating  
XX PT production of nitric oxide - by administration of vascular  
XX PT endothelial growth factor, useful for, e.g. treating or preventing  
XX PT intimal hyperplasia  
XX XX  
XX PS Claim 8; Pages 56-57; 70pp; English.  
XX XX  
XX CC The present sequence represents human vascular endothelial growth factor  
XX CC 165 (VEGF-165). VEGF stimulates production of nitric oxide and  
XX CC prostacyclin. VEGF can therefore be used for treatment or prevention  
XX CC of intimal hyperplasia in a blood vessel. VEGF can be used for treating  
XX CC or preventing any condition responsive to in vivo stimulation of  
XX CC nitric acid and prostacyclin (especially essential hypertension,  
XX CC pulmonary arterial hypertension (PAH), cor pulmonale and  
XX CC atherosclerosis. VEGF is specifically used to control (re)stenosis,  
XX CC where caused by PAH or by a surgical procedure such as angioplasty,  
XX CC coronary bypass operation, anastomosis or endarterectomy.  
XX XX  
XX SQ Sequence 191 AA;  
Query Match 100.0%; Score 792; DB 19; Length 191;  
Best Local Similarity 100.0%; Pred. No. 1.1e-75;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MNFLSWHWSLALLLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
Qy 61 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLECYPTESNITMQIMRIKPHQGHIGEM 120  
Db 61 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLECYPTESNITMQIMRIKPHQGHIGEM 120  
Qy 121 SFLQHNKCECRPKKDRARQEK 141  
Db 121 SFLQHNKCECRPKKDRARQEK 141  
RESULT 15  
AA43483  
ID AAY43483 standard; Protein; 208 AA.  
XX AC AAY43483;  
XX XX  
XX DT 26-JAN-2000 (first entry)  
XX XX

DE XX Amino acid sequence of VEGF-A182 protein.  
XX KW Vascular endothelial factor; VEGF; VEGF-A182; variant; vascular disease;  
XX KW cardiovascular disease; vascular cell proliferation; angioplasty;  
XX KW restenosis; drug permeation; tumour; ischemic condition;  
XX KW cardiac infarction; chronic coronary ischemia; stroke; wound treatment;  
XX KW chronic lower limb ischemia; peripheral vascular disease.  
XX OS Homo sapiens.  
XX XX  
XX FH Key Location/Qualifiers  
XX FT Peptide 1..27  
XX FT /note= "secretion signal sequence"  
XX PN WO9940197-A2.  
XX PD 12-AUG-1999.  
XX PF 04-FEB-1999; 99WO-US02425.  
XX PR 06-FEB-1998; 98US-0073979.  
XX XX  
XX PA (COLL-) COLLATERAL THERAPEUTICS INC.  
XX XX  
XX PI Baird A, Andreason G;  
XX XX  
XX DR WPI; 1999-600967/51.  
XX DR N-PSDB; RAZ29997.  
XX XX  
XX PT New growth factor variants, useful for treating cardiovascular disease,  
XX PT especially by stimulating vascular cell proliferation -  
XX XX  
XX PS Claim 8; Fig 4; 101pp; English.  
XX XX  
XX CC The present sequence represents vascular endothelial factor VEGF-A182.  
XX CC It is a VEGF-A variant of the invention. The specification describes new  
XX CC VEGF-A variants in which exon 6a is excluded (other forms which contain  
XX CC both exon 6a and 6b are also described). The variants have a modified  
XX CC affinity for matrix and low affinity receptors. This alters the  
XX CC bioavailability of the proteins when administered directly to cells.  
XX CC These variants are used to treat vascular disease, especially  
XX CC cardiovascular disease, by stimulating vascular cell proliferation. They  
XX CC enhance epithelialisation of diseased vessels, especially after  
XX CC angioplasty. The re-endothelialisation reduces or prevents restenosis.  
XX CC They are also useful for enhancing drug permeation by tumours and for  
XX CC treating ischemic conditions such as cardiac infarction, chronic coronary  
XX CC ischemia, chronic lower limb ischemia, stroke and peripheral vascular  
XX CC disease. In addition they may be used to treat wounds.  
XX XX  
XX SQ Sequence 208 AA;  
Query Match 100.0%; Score 792; DB 20; Length 208;  
Best Local Similarity 100.0%; Pred. No. 1.3e-75;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MNFLSWHWSLALLLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
Db 1 MNFLSWHWSLALLLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
Qy 61 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLECYPTESNITMQIMRIKPHQGHIGEM 120  
Db 61 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLECYPTESNITMQIMRIKPHQGHIGEM 120  
Qy 121 SFLQHNKCECRPKKDRARQEK 141  
Db 121 SFLQHNKCECRPKKDRARQEK 141

Search completed: November 20, 2002, 04:56:32  
Job time : 83 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 04:56:43 ; Search time 51 Seconds  
(without alignments)  
43.299 Million cell updates/sec

Title: US-09-884-050-2

Perfect score: 792

Sequence: 1 MNFLSWHWSLALLYLHH.....FLQHNKCECRPKKDRARQEK 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PublishedApplications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*
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- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB pep.\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	792	100.0	171	10	US-09-812-133-2
2	792	100.0	215	10	US-09-244-694-3
3	792	100.0	232	10	US-09-795-006A-147
4	792	100.0	232	12	US-10-127-551-5
5	787	99.4	191	10	US-09-349-954A-2
6	787	99.4	191	10	US-09-932-451A-2
7	787	99.4	191	10	US-09-907-007-2
8	787	99.4	191	10	US-09-795-006A-2
9	787	99.4	192	9	US-09-852-209A-8
10	686.5	86.7	214	10	US-09-349-954A-22
11	686.5	86.7	214	10	US-09-907-007-22
12	645	81.4	190	9	US-09-813-398-8
13	621	78.4	110	10	US-09-822-270-17
14	583	73.6	126	10	US-09-795-006A-43
15	531	67.0	94	10	US-09-761-636A-2
16	521.5	65.8	127	10	US-09-795-006A-83
17	516	65.2	105	10	US-09-925-299-927
18	512.5	64.7	127	10	US-09-795-006A-87
19	506	63.9	105	10	US-09-795-006A-51

20	501	63.3	126	10	US-09-795-006A-55	Sequence 55, Appl
21	474.5	59.9	127	10	US-09-795-006A-91	Sequence 91, Appl
22	465.5	58.8	127	10	US-09-795-006A-95	Sequence 95, Appl
23	460.5	58.1	127	10	US-09-795-006A-85	Sequence 85, Appl
24	459	58.0	105	10	US-09-795-006A-59	Sequence 59, Appl
25	454	57.3	126	10	US-09-795-006A-63	Sequence 63, Appl
26	452	57.1	105	10	US-09-795-006A-153	Sequence 153, Appl
27	451.5	57.0	127	10	US-09-795-006A-89	Sequence 89, Appl
28	451	56.9	79	9	US-10-086-623-14	Sequence 14, Appl
29	449.5	56.8	105	10	US-09-795-006A-161	Sequence 161, Appl
30	449	56.7	126	10	US-09-795-006A-53	Sequence 53, Appl
31	445.5	56.2	129	10	US-09-795-006A-99	Sequence 99, Appl
32	440	55.6	126	10	US-09-795-006A-57	Sequence 57, Appl
33	436.5	55.1	129	10	US-09-795-006A-103	Sequence 103, Appl
34	434	54.8	128	10	US-09-795-006A-67	Sequence 67, Appl
35	425	53.7	128	10	US-09-795-006A-71	Sequence 71, Appl
36	415	52.4	105	10	US-09-795-006A-173	Sequence 173, Appl
37	413.5	52.2	127	10	US-09-795-006A-93	Sequence 93, Appl
38	413	52.1	105	10	US-09-795-006A-163	Sequence 163, Appl
39	406	51.3	105	10	US-09-795-006A-175	Sequence 175, Appl
40	404.5	51.1	127	10	US-09-795-006A-97	Sequence 97, Appl
41	402	50.8	126	10	US-09-795-006A-61	Sequence 61, Appl
42	398.5	50.3	129	10	US-09-795-006A-107	Sequence 107, Appl
43	393	49.6	105	10	US-09-795-006A-165	Sequence 165, Appl
44	393	49.6	126	10	US-09-795-006A-65	Sequence 65, Appl
45	390	49.2	128	10	US-09-795-006A-45	Sequence 45, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-812-133-2  
; Sequence 2, Application US/09812133  
; Patent No. US20020065240A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Kenneth A., Jr.  
; APPLICANT: Kendall, Richard L.  
; APPLICANT: Bett, Andrew J.  
; APPLICANT: Huckle, William R.  
; TITLE OF INVENTION: GENE THERAPY FOR STIMULATION OF ANGIOGENESIS  
; FILE REFERENCE: 20073P  
; CURRENT APPLICATION NUMBER: US/09/812,133  
; CURRENT FILING DATE: 2001-03-19  
; PRIOR APPLICATION NUMBER: PCT/US98/22668  
; PRIOR FILING DATE: 1998-10-23  
; PRIOR APPLICATION NUMBER: 60/063,629  
; PRIOR FILING DATE: 1997-10-27  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID, NO 2  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: Human  
US-09-812-133-2

Query Match 100.0%; Score 792; DB 10; Length 171;  
Best Local Similarity 100.0%; Pred. No. 1.4e-75;  
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNFLSWHWSLALLYLHHAKWSQAAPMAEGGCGCCNDGECVPTESNITMIRKPHQGHIGM	60
Db	1	MNFLSWHWSLALLYLHHAKWSQAAPMAEGGCGCCNDGECVPTESNITMIRKPHQGHIGM	60
Qy	61	IFQEYPTDEITYFKSCVPLMRCGGCCNDGECVPTESNITMIRKPHQGHIGM	120
Db	61	IFQEYPTDEITYFKSCVPLMRCGGCCNDGECVPTESNITMIRKPHQGHIGM	120
Qy	121	SFLQHNKCECRPKKDRARQEK	141
Db	121	SFLQHNKCECRPKKDRARQEK	141

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RESULT 2
US-09-244-694-3
; Sequence 3, Application US/09244694
; Patent No. US20020026037A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Jing-Shan
; APPLICANT: Olsen, Henrik S.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor 3
; FILE REFERENCE: 1488.1040003
; CURRENT APPLICATION NUMBER: US/09/244,694
; CURRENT FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: US 09/132,088
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: US 09/033,662
; EARLIER FILING DATE: 1998-03-03
; EARLIER APPLICATION NUMBER: US 08/469,641
; EARLIER FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-244-694-3

Query Match      100.0%; Score 792; DB 10; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.8e-75;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNFLLSVHWHSALLLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLYD 60
QY 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDGEGLECVPTESNTMTQIMRIKPHQGQHIGEM 120
Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDGEGLECVPTESNTMTQIMRIKPHQGQHIGEM 120
QY 121 SFLOHNKCECRPKKDRARQEK 141
Db 121 SFLOHNKCECRPKKDRARQEK 141

RESULT 3
US-09-795-006A-147
; Sequence 147, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 147
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-006A-147

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Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDGEGLECVPTESNTMTQIMRIKPHQGQHIGEM 120
QY 121 SFLOHNKCECRPKKDRARQEK 141
Db 121 SFLOHNKCECRPKKDRARQEK 141

RESULT 4
US-10-127-551-5
; Sequence 5, Application US/10127551
; Patent No. US20020120123A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor 2
; FILE REFERENCE: PF112P1
; CURRENT APPLICATION NUMBER: US/10/127,551
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/465,968
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/207,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-127-551-5

Query Match      100.0%; Score 792; DB 12; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.9e-75;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLLSVHWHSALLLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLYD 60
Db 1 MNFLLSVHWHSALLLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLYD 60
QY 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDGEGLECVPTESNTMTQIMRIKPHQGQHIGEM 120
Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDGEGLECVPTESNTMTQIMRIKPHQGQHIGEM 120
QY 121 SFLOHNKCECRPKKDRARQEK 141
Db 121 SFLOHNKCECRPKKDRARQEK 141

RESULT 5
US-09-349-954A-2
; Sequence 2, Application US/09349954A
; Patent No. US20020019027A1
; GENERAL INFORMATION:
; APPLICANT: Hayward, Nicholas K.
; APPLICANT: Weber, Gunther
; APPLICANT: Grimmond, Sean
; APPLICANT: No. US20020019027Aldenskjold, Magnus
; APPLICANT: Larsson, Catharina
; TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
; FILE REFERENCE: Dav. Col. Cave
; CURRENT APPLICATION NUMBER: US/09/349,954A
; CURRENT FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 08/765,588
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Nucleotide Sequence of VEGF165
US-09-349-954A-2

; Sequence 2, Application US/09349954A
; Patent No. US20020019027A1
; GENERAL INFORMATION:
; APPLICANT: Hayward, Nicholas K.
; APPLICANT: Weber, Gunther
; APPLICANT: Grimmond, Sean
; APPLICANT: No. US20020019027Aldenskjold, Magnus
; APPLICANT: Larsson, Catharina
; TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING
; FILE REFERENCE: Dav. Col. Cave
; CURRENT APPLICATION NUMBER: US/09/349,954A
; CURRENT FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 08/765,588
; PRIOR FILING DATE: 1996-02-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Nucleotide Sequence of VEGF165
US-09-349-954A-2
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## US-09-349-954A-2

Query Match 99.4%; Score 787; DB 10; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.1e-75;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
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Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHOGHIGEM 120  
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Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHOGHIGEM 120  
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Qy 121 SFLQHNKCECRPKKDRARQE 140  
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Db 121 SFLQHNKCECRPKKDRARQE 140  
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## RESULT 6

US-09-932-451A-2  
; Sequence 2, Application US/09932451A  
; Patent No. US2002011324A1  
; GENERAL INFORMATION:  
; APPLICANT: OZAWA, Kelya  
; APPLICANT: SHIMPO, Masahisa  
; APPLICANT: IKEDA, Uichi  
; APPLICANT: MAEDA, Yoshikazu  
; APPLICANT: SHIMADA, Kazuyuki  
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-MEDIATED DELIVERY OF ANGIOGENIC  
; FILE REFERENCE: 0800-0026  
; CURRENT APPLICATION NUMBER: US/09/932,451A  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/226,056  
; PRIOR FILING DATE: 2000-08-17  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VEGF-165

## US-09-932-451A-2

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Best Local Similarity 100.0%; Pred. No. 5.1e-75;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
|||||

Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHOGHIGEM 120  
|||||  
Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHOGHIGEM 120  
|||||

Qy 121 SFLQHNKCECRPKKDRARQE 140  
|||||  
Db 121 SFLQHNKCECRPKKDRARQE 140  
|||||

## RESULT 7

US-09-907-007-2  
; Sequence 2, Application US/09907007  
; Patent No. US20020142395A1  
; GENERAL INFORMATION:  
; APPLICANT: Hayward, Nicholas K.  
; APPLICANT: Weber, Gunther  
; APPLICANT: Grimmond, Sean  
; APPLICANT: No. US20020142395A1denskjold, Magnus  
; APPLICANT: Larsson, Catharina

; TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING  
; FILE REFERENCE: SAME  
; CURRENT APPLICATION NUMBER: US/09/907,007  
; CURRENT FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: 08/765,588  
; PRIOR FILING DATE: 1996-02-22  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Nucleotide Sequence of VEGF165  
US-09-907-007-2

Query Match 99.4%; Score 787; DB 10; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.1e-75;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHOGHIGEM 120  
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Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHOGHIGEM 120  
|||||

Qy 121 SFLQHNKCECRPKKDRARQE 140  
|||||  
Db 121 SFLQHNKCECRPKKDRARQE 140  
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## RESULT 8

US-09-795-006A-2  
; Sequence 2, Application US/09795006A  
; Patent No. US20020151680A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo et al  
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR  
; FILE REFERENCE: 28967/35977B  
; CURRENT APPLICATION NUMBER: US/09/795,006A  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: US 60/205,331  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: US 60/185,205  
; PRIOR FILING DATE: 2000-02-25  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 191  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-795-006A-2

Query Match 99.4%; Score 787; DB 10; Length 191;  
Best Local Similarity 100.0%; Pred. No. 5.1e-75;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
|||||  
Db 1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
|||||

Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHOGHIGEM 120  
|||||  
Db 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHOGHIGEM 120  
|||||

Qy 121 SFLQHNKCECRPKKDRARQE 140  
|||||  
Db 121 SFLQHNKCECRPKKDRARQE 140  
|||||

## RESULT 9



; FILE REFERENCE: UOFMD.003C1  
; CURRENT APPLICATION NUMBER: US/09/813,398  
; CURRENT FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: PCT/US99/05908  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: PCT/US98/19772  
; PRIOR FILING DATE: 1998-09-22  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: HOMO SAPIEN  
; US-09-813-398-8

Query Match 81.4%; Score 645; DB 9; Length 190;  
Best Local Similarity 100.0%; Pred. No. 3.2e-60;  
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 APMAEGGQNHHEVVKFMDVYQSYCHPIETLVDFIQEYDPEIEYIFKPSVPLMRCGGC 86

Db 2 APMAEGGQNHHEVVKFMDVYQSYCHPIETLVDFIQEYDPEIEYIFKPSVPLMRCGGC 61

QY 87 CNDEGLECVPTESNITMQIMRIKPHOGQHIGEMSFLOHKNKCECRPKKDRARQEK 141

Db 62 CNDEGLECVPTESNITMQIMRIKPHOGQHIGEMSFLOHKNKCECRPKKDRARQEK 116

## RESULT 13

US-09-822-270-17

; Sequence 17, Application US/09822270

; Patent No. US20020068697A1

; GENERAL INFORMATION:

; APPLICANT: TOURNARE, ROSELYNE

; APPLICANT: DEMANGEL, CAROLINE

; APPLICANT: DERBIN, CLAUDE

; APPLICANT: PERRET, GERARD

; APPLICANT: MAZIE, JEAN-CLAUDE

; APPLICANT: PLOUET, JEAN

; APPLICANT: VASSAY, ROGER

; TITLE OF INVENTION: PEPTIDES BLOCKING VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-MEDIATED

; TITLE OF INVENTION: ANGIOGENESIS, POLYNUCLEOTIDES ENCODING SAID PEPTIDES AND METHODS

; FILE REFERENCE: 2050600S0

; CURRENT APPLICATION NUMBER: US/09/822,270

; CURRENT FILING DATE: 2001-04-02

; PRIOR APPLICATION NUMBER: US 60/193,396

; PRIOR FILING DATE: 2000-03-31

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 17

; LENGTH: 110

; TYPE: PRT

; ORGANISM: ARTIFICIAL SEQUENCE

; FEATURE:

; OTHER INFORMATION: SYNTHETIC PEPTIDE

; US-09-822-270-17

Query Match 78.4%; Score 621; DB 10; Length 110;  
Best Local Similarity 100.0%; Pred. No. 5.4e-58;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 APMAEGGQNHHEVVKFMDVYQSYCHPIETLVDFIQEYDPEIEYIFKPSVPLMRCGGC 86

Db 1 APMAEGGQNHHEVVKFMDVYQSYCHPIETLVDFIQEYDPEIEYIFKPSVPLMRCGGC 60

QY 87 CNDEGLECVPTESNITMQIMRIKPHOGQHIGEMSFLOHKNKCECRPKKDR 136

Db 61 CNDEGLECVPTESNITMQIMRIKPHOGQHIGEMSFLOHKNKCECRPKKDR 110

## RESULT 14

US-09-795-006A-43

; Sequence 43, Application US/09795006A

; Patent No. US20020151680A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo et al  
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR  
; FILE REFERENCE: 28967/35977B  
; CURRENT APPLICATION NUMBER: US/09/795,006A  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: US 60/205,331  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: US 60/185,205  
; PRIOR FILING DATE: 2000-02-25  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 43  
; LENGTH: 126  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence of hy  
; OTHER INFORMATION: DNA  
; US-09-795-006A-43

Query Match 73.6%; Score 583; DB 10; Length 126;

Best Local Similarity 95.4%; Pred. No. 5.8e-54;

Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 34 GQNHHEVVKFMDVYQSYCHPIETLVDFIQEYDPEIEYIFKPSVPLMRCGGCCNDEGLE 93

Db 1 GQNHHEVVKFMDVYQSYCHPIETLVDFIQEYDPEIEYIFKPSVPLMRCGGCCNDEGLE 60

QY 94 CVPTESNITMQIMRIKPHOGQHIGEMSFLOHKNKCECRPKKDRARQEK 141

Db 61 CVPTESNITMQIMRIKPHOGQHIGEMSFLOHKNKCECRPKKDLVPEQK 108

## RESULT 15

US-09-761-636A-2

; Sequence 2, Application US/09761636A

; Patent No. US20020065218A1

; GENERAL INFORMATION:

; APPLICANT: ACHEN, Marc

; APPLICANT: STACKER, Steven

; APPLICANT: HUGHES, Richard

; APPLICANT: CENDRON, Angela

; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

; FILE REFERENCE: 1064/48505 Achen et al

; CURRENT APPLICATION NUMBER: US/09/761,636A

; CURRENT FILING DATE: 2001-01-18

; PRIOR APPLICATION NUMBER: US 60/176,293

; PRIOR FILING DATE: 2000-01-18

; PRIOR APPLICATION NUMBER: US 60/204,590

; PRIOR FILING DATE: 2000-05-16

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 94

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc-feature

; OTHER INFORMATION: Amino acid residues Lys42-Asp135 of VEGF165

; US-09-761-636A-2

Query Match 67.0%; Score 531; DB 10; Length 94;

Best Local Similarity 98.9%; Pred. No. 1.1e-48;

Matches 93; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 42 KFMDVYQSYCHPIETLVDFIQEYDPEIEYIFKPSVPLMRCGGCCNDEGLECVPTESN 101

Db 1 KFMDVYQSYCHPIETLVDFIQEYDPEIEYIFKPSVPLMRCGGCCNDEGLECVPTESN 60

QY 102 ITMQIMRIKPHOGQHIGEMSFLOHKNKCECRPKKD 135

Db 61 :|||||||||||||||||||||||||||||||||||||  
LTMQIMRIKPHOGHIGEMSFLQHNKCECRPKD 94

Search completed: November 20, 2002, 05:01:37  
Job time : 52 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 04:55:04 ; Search time 45 Seconds  
(without alignments)  
301.221 Million cell updates/sec

Title: US-09-884-050-2

Perfect score: 792

Sequence: 1 MNFLSWHWSLALLYLHH.....FLOHNRCEPRKKDRARQEK 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_73.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	792	100.0	232	2 A41551	vascular endotheli
2	733.5	92.6	190	2 S52130	vascular endotheli
3	719.5	90.8	146	2 S57956	ovine vascular end
4	717.5	90.6	190	2 B40080	vascular endotheli
5	686.5	86.7	214	2 A44881	vascular endotheli
6	681.5	86.0	190	2 B44881	vascular endotheli
7	680.5	85.9	190	2 A35987	glioma-derived vas
8	575.5	72.7	120	2 A33787	vascular endotheli
9	367.5	46.4	128	2 I51295	vascular endotheli
10	325	41.0	149	2 A41236	placental growth f
11	294	37.1	158	2 A56125	placental growth f
12	264	33.3	188	2 JC4680	vascular endotheli
13	264	33.3	207	2 JC4679	vascular endotheli
14	237	29.9	133	2 B49530	vascular endotheli
15	192	24.2	419	2 S69207	vascular endotheli
16	163	20.6	148	2 D49530	16K vascular endot
17	137.5	17.4	36	2 A60706	vascular endotheli
18	99.5	12.6	226	1 TVMVSS	PDGF-related trans
19	99.5	12.6	241	1 PFHUG2	platelet-derived g
20	99.5	12.6	245	1 TVCTSS	platelet-derived g
21	96.5	12.2	200	2 I51551	platelet-derived g
22	96.5	12.2	215	2 S08220	platelet-derived g
23	96.5	12.2	226	2 I51550	platelet-derived g
24	95	12.0	211	1 PFHUG1	platelet-derived g
25	94.5	11.9	166	2 JN0248	platelet-derived g
26	94.5	11.9	196	2 B28964	platelet-derived g
27	94.5	11.9	196	2 A48851	platelet-derived g
28	94.5	11.9	197	2 S25096	platelet-derived g
29	94.5	11.9	198	2 JS0735	platelet-derived g

#### ALIGNMENTS

##### RESULT 1

A41551

vascular endothelial growth factor 206 precursor - human  
N:Alternate names: vascular permeability factor  
N:Contains: vascular endothelial growth factor 121 (VEGF 121); VEGF 165; VEGF 189; VE

C:Species: Homo sapiens (man)

C:Date: 28-Aug-1992 #sequence.revision 28-Aug-1992 #text.change 05-Nov-1999  
C:Accession: A41551; C41551; B41551; A40454; B40454; A40079; A40080; JQ1463

R:Houck, K.A.; Ferrara, N.; Winer, J.; Cachianes, G.; Li, B.; Leung, D.W.

Mol. Endocrinol. 5, 1806-1814, 1991

A:Title: The vascular endothelial growth factor family: identification of a fourth mo  
A:Reference number: A41551; MUID:92168017; PMID:1791831

A:Accession: A41551

A:Molecule type: mRNA

A:Residues: 1-232 <H0U1>

A:Cross-references: GB:S85192; NID:g246155; PID:g246156

A:Accession: C41551

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-140, 'N', 183-232 <H0U2>

A:Accession: B41551  
A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-141, 227-232 <H0U>

R:Tischer, E.; Mitchell, R.; Hartman, T.; Silva, M.; Gospodarowicz, D.; Fiddes, J.C.;

J. Biol. Chem. 266, 11947-11954, 1991

A:Title: The human gene for vascular endothelial growth factor. Multiple protein form

A:Reference number: A40454; MUID:91268072; PMID:1711045

A:Accession: A40454

A:Molecule type: DNA

A:Residues: 1-165, 183-232 <T11>

A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63976;

A:Accession: B40454

A:Molecule type: DNA

A:Residues: 1-140, 'N', 183-232 <T12>

A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63977;

A:Accession: C40454

A:Molecule type: DNA

A:Residues: 1-141, 227-232 <T13>

A:Cross-references: GB:M63971; GB:M63972; GB:M63973; GB:M63974; GB:M63975; GB:M63978

R:Kock, P.J.; Hauser, S.D.; Krivi, G.; Sanzo, K.; Warren, T.; Feder, J.; Connolly, D.

Science 246, 1309-1312, 1989

A:Title: Vascular permeability factor, an endothelial cell mitogen related to PDGF.

A:Reference number: A40079; MUID:90069609; PMID:2479987

A:Accession: A40079

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-165, 183-232 <KEC>

A:Cross-references: GB:M27281; NID:g340300; PIDN:AAA36807.1; PID:g340301

R:Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.

Science 246, 1306-1309, 1989

A:Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.

A:Reference number: A40080; MUID:90069608; PMID:2479986  
A:Accession: B40080  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-140, 'N', 183-232 <LEU>  
A:Cross-references: GB:M32977; NID:g181970; PIDN:AAA35789.1; PID:g181971  
R:Weinidel, K.; Marne, D.; Welch, H.A.  
Biochem. Biophys. Res. Commun. 183, 1167-1174, 1992  
A:Title: AIDS-associated Kaposi's sarcoma cells in culture express vascular endothelial  
A:Reference number: JQ1463; MUID:92231879; PMID:1567395  
A:Accession: JQ1463  
A:Molecule type: mRNA  
A:Residues: 1-140, 'N', 183-232 <WEI>  
A:Cross-references: EMBL:X62568; NID:g37658; PIDN:CAA44447.1; PID:g37659  
A:Experimental source: AIDS-Kaposi's sarcoma cell  
A:Accession: JQ1464  
A:Molecule type: mRNA  
A:Residues: 1-140, 'N', 227-232 <WE2>  
A:Experimental source: AIDS-Kaposi's sarcoma cell  
R:Connolly, D.T.; Olander, J.V.; Heuvelman, D.; Nelson, R.; Monsell, R.; Siegel, N.; Hay  
J. Biol. Chem. 264, 20017-20024, 1989  
A:Title: Human vascular permeability factor. Isolation from U937 cells.  
A:Reference number: A34492; MUID:90062112; PMID:2584205  
A:Accession: A34492  
A:Molecule type: protein  
A:Residues: 27-36; 43-49, 'R', 72-76, 'Q', 78-81; 59-71 <CON>  
C:Comment: The most common of several alternatively spliced forms is VEGF 165.  
C:Genetics:  
A:Gene: GDB:VEGF  
A:Cross-references: GDB:132244; OMIM:192240  
A:Map position: 6p21-6p12  
C:Function:  
A:Description: promotes fluid and protein leakage from blood vessels  
C:Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; extracellular pro  
F:1-232/Product: vascular endothelial growth factor 206 precursor #status predicted <V20  
F:1-165, 183-232/Product: vascular endothelial growth factor 189 precursor #status predic  
F:1-141, 227-232/Product: vascular endothelial growth factor 121 precursor #status predic  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 792; DB 2; Length 232;  
Best Local Similarity 100.0%; Pred. No. 9e+73; Indels 0; Gaps 0;  
Matches 141; Conservative 0; Mismatches 0;

QY 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVFMDVYQSYCHPIETLVD 60  
|||||  
Db 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVFMDVYQSYCHPIETLVD 60  
|||||

QY 61 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
|||||  
Db 61 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
|||||

QY 121 SFLOHNKCECRPKDKARQEK 141  
|||||  
Db 121 SFLOHNKCECRPKDKARQEK 141  
|||||

RESULT 2  
S52130  
vascular endothelial growth factor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 05-Nov-1999  
C:Accession: S52130  
R:Sharma, H.S.; Tang, Z.H.; Cho, B.C.G.; Verdouw, P.D.  
Biochim. Biophys. Acta 1260, 235-238, 1995  
A:Title: Nucleotide sequence and expression of the porcine vascular endothelial growth  
A:Reference number: S52130; MUID:95143284; PMID:7841203  
A:Accession: S52130  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-190 <SHA>  
A:Cross-references: GB:X81380; NID:g587559; PIDN:CAA57143.1; PID:g587560

Query Match 92.6%; Score 733.5; DB 2; Length 190;  
Best Local Similarity 95.7%; Pred. No. 6.2e-67;  
Matches 134; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVFMDVYQSYCHPIETLVD 60  
|||||  
Db 1 MNFLSWHWSLALLYLHAKWSQAAPMAE-GGQKPEHVVFMDVYQSYCHPIETLVD 59  
|||||

QY 61 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
|||||  
Db 60 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 119  
|||||

QY 121 SFLOHNKCECRPKDKARQEK 140  
|||||  
Db 120 SFLOHNKCECRPKDKARQEK 139  
|||||

RESULT 3  
S57956  
ovine vascular endothelial growth factor - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C>Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 05-Nov-1999  
C:Accession: S57956  
R:Redmer, D.A.; Dai, Y.; Li, J.; Jones, S.C.; Moor, R.M.  
submitted to the EMBL Data Library, July 1995  
A:Reference number: S57956  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-146 <RED>  
A:Cross-references: EMBL:X89506; NID:g899350; PIDN:CAA61677.1; PID:g899351

Query Match 90.8%; Score 719.5; DB 2; Length 146;  
Best Local Similarity 92.2%; Pred. No. 1.2e-65;  
Matches 130; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGQNHHEVVFMDVYQSYCHPIETLVD 60  
|||||  
Db 1 MNFLSWHWSLALLYLHAKWSQAAPMAE-GGQKPEHVVFMDVYQSYCHPIETLVD 59  
|||||

QY 61 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHQGQHIGEM 120  
|||||  
Db 60 IFQEYPDEIEYIFKPSVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHOSQHIGEM 119  
|||||

QY 121 SFLOHNKCECRPKDKARQEK 141  
|||||  
Db 120 SFLOHNKCECRPKDKARQEK 140  
|||||

RESULT 4  
B40080  
vascular endothelial growth factor precursor (version 2) - bovine  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 05-Nov-1999  
C:Accession: B40080; B33787; A33255  
R:Leung, D.W.; Cachianes, G.; Kuang, W.J.; Goeddel, D.V.; Ferrara, N.  
Science 246, 1306-1309, 1989  
A:Title: Vascular endothelial growth factor is a secreted angiogenic mitogen.  
A:Reference number: A40080; MUID:90069608; PMID:2479986  
A:Accession: B40080  
A:Molecule type: mRNA  
A:Residues: 1-190 <LEU>  
A:Cross-references: GB:M32976; NID:g163006; PIDN:AAA30502.1; PID:g163007  
R:Tischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Cr  
Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989  
A:Title: Vascular endothelial growth factor: a new member of the platelet-derived gro  
A:Reference number: A33787; MUID:90121225; PMID:2610687  
A:Accession: B33787  
A:Molecule type: mRNA  
A:Residues: 27-190 <TIS>  
A:Cross-references: GB:M31836; NID:g163808; PIDN:AAA30804.1; PID:g163809  
R:Ferrara, N.; Henzel, W.J.  
Biochem. Biophys. Res. Commun. 161, 851-858, 1989

A>Title: Pituitary follicular cells secrete a novel heparin-binding growth factor specific  
 A:Reference number: A33255; MUID:89286596; PMID:2735925

A:Molecule type: protein  
 A:Residues: 27-31 <FER>  
 C:Keywords: alternative splicing; glycoprotein  
 F:1-26/Domain: signal sequence #status predicted <SIG>  
 F:27-190/Product: vascular endothelial growth factor #status predicted <MAT>  
 F:100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.6%; Score 717.5; DB 2; Length 190;  
 Best Local Similarity 92.9%; Pred. No. 2.6e-65;  
 Matches 130; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Qy 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1 MNFLSWHWSLALLYLHHAKWSQAAPMAE-GGQKPEHVVKFMDVYORSYCHPIETLVD 59  
 Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRKPHQGHIGEM 120  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 60 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRKPHQGHIGEM 119  
 Qy 121 SFLQHNKCECRPKKDRARQE 140  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 120 SFLQHNKCECRPKKDRARQE 139

## RESULT 5

A44881

vascular endothelial growth factor-3 precursor - mouse  
 N:Contains: vascular endothelial growth factor-2; vascular permeability factor  
 C:Species: Mus musculus (house mouse)  
 C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 08-Oct-1999  
 C:Accession: A44881; A460932; S52136  
 R:Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.  
 Development 114, 521-532, 1992

A>Title: Expression of vascular endothelial growth factor during embryonic angiogenesis  
 A:Reference number: A44881; MUID:92274860; PMID:1592003

A:Accession: A44881  
 A:Molecule type: mRNA  
 A:Residues: 1-214 <BRE>  
 A:Cross-references: GB:S37052; NID:g249856; PIDN:AB22252.1; PID:g249857  
 A:Note: sequence extracted from NCBI backbone (NCBIN:104677, NCBI:P:104678)  
 A:Experimental source: embryo  
 A:Accession: C44881

A:Molecule type: protein  
 A:Residues: 1-140, 209-214 <BR2>  
 A:Cross-references: GB:S38100; NID:g249860; PIDN:AB22254.1; PID:g249861  
 A:Note: sequence extracted from NCBI backbone (NCBIN:107624, NCBI:P:107625)  
 R:Clauss, M.; Gerlach, M.; Gerlach, H.; Brett, J.; Wang, F.; Familletti, P.C.; Pan, Y.C.  
 J. Exp. Med. 172, 1535-1545, 1990  
 A>Title: Vascular permeability factor: a tumor-derived polypeptide that induces endothelial

A:Reference number: A60932; MUID:91079755; PMID:2258694  
 A:Accession: A60932  
 A:Molecule type: protein  
 A:Residues: 27-33 <CLA>  
 R:Sugihara, T.; Kaul, S.C.; Mitsui, Y.; Wadhwa, R.  
 Biochim. Biophys. Acta 1224, 365-370, 1994  
 A>Title: Enhanced expression of multiple forms of VEGF is associated with spontaneous in

A:Reference number: S52136; MUID:95101726; PMID:7803491  
 A:Accession: S52136  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 27-46 <SUG>

C:Comment: Homodimers could be demonstrated for recombinant VEGF-2 but not VEGF-3.  
 C:Keywords: alternative splicing; angiogenesis; disulfide bond; glycoprotein; homodimer;  
 F:1-26/Domain: signal sequence #status predicted <SIG>  
 F:27-214/Product: vascular endothelial growth factor-3 #status experimental <MAT>

Query Match 86.7%; Score 686.5; DB 2; Length 214;  
 Best Local Similarity 87.2%; Pred. No. 4.1e-62;  
 Matches 123; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

Qy 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1 MNFLSWHWSLALLYLHHAKWSQAAPTE-GEQKSHSEVVKFMDVYORSYCHPIETLVD 59  
 Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRKPHQGHIGEM 120  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 60 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRKPHQGHIGEM 119  
 Qy 121 SFLQHNKCECRPKKDRARQE 141  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 120 SFLQHSRCECRPKKDRTRPEK 140

## RESULT 6

B44881

vascular endothelial growth factor-1 precursor - mouse

C:Species: Mus musculus (house mouse)  
 C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 05-Nov-1999  
 C:Accession: B44881; A43351; A61029  
 R:Breier, G.; Albrecht, U.; Sterrer, S.; Risau, W.  
 Development 114, 521-532, 1992

A>Title: Expression of vascular endothelial growth factor during embryonic angiogenesis  
 A:Reference number: A44881; MUID:92274860; PMID:1592003

A:Accession: B44881

A:Molecule type: mRNA

A:Residues: 1-190 &lt;BRE&gt;

A:Cross-references: GB:S38083; NID:g249858; PIDN:AB22253.1; PID:g249859

A:Experimental source: embryo

A:Note: sequence extracted from NCBI backbone (NCBIN:107622, NCBI:P:107623)

R:Claiffey, K.P.; Wilkison, W.O.; Spiegelman, B.M.

J. Biol. Chem. 267, 16317-16322, 1992

A>Title: Vascular endothelial growth factor. Regulation by cell differentiation and a  
 A:Reference number: A43351; MUID:92355593; PMID:1644816

A:Accession: A43351

A:Molecule type: mRNA

A:Residues: 1-116, 191-190 &lt;CLA&gt;

A:Cross-references: GB:M95200; NID:g202350; PIDN:AAA0547.1; PID:g202351

A:Note: sequence extracted from NCBI backbone (NCBIN:110665, NCBI:P:110675)

R:Rosenthal, R.A.; Megyesi, J.F.; Henzel, W.J.; Ferrara, N.; Folkman, J.

Growth Factors 4, 53-59, 1990

A>Title: Conditioned medium from mouse sarcoma 180 cells contains vascular endothelial  
 A:Reference number: A61029; MUID:91197543; PMID:2085441

A:Accession: A61029

A:Molecule type: protein

A:Residues: 27-38 &lt;ROS&gt;

C:Keywords: alternative splicing; angiogenesis; dimer; disulfide bond; glycoprotein;  
 Query Match 86.0%; Score 681.5; DB 2; Length 190;  
 Best Local Similarity 87.1%; Pred. No. 1.2e-61;  
 Matches 122; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

Qy 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYORSYCHPIETLVD 60  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 1 MNFLSWHWSLALLYLHHAKWSQAAPTE-GEQKSHSEVVKFMDVYORSYCHPIETLVD 59

Qy 61 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRKPHQGHIGEM 120  
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
 Db 60 IFQEYPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRKPHQGHIGEM 119

Qy 121 SFLQHNKCECRPKKDRARQE 140

|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 120 SFLQHSRCECRPKKDRTRPE 139

## RESULT 7

A35987

glioma-derived vascular endothelial cell growth factor - rat

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 16-Nov-1990 #sequence\_revision 16-Nov-1990 #text\_change 05-Nov-1999

C:Accession: A35987

R:Conn, G.; Bayne, M.L.; Soderman, D.D.; Kwok, P.W.; Sullivan, K.A.; Palisi, T.M.; Ho  
 Proc. Natl. Acad. Sci. U.S.A. 87, 2628-2632, 1990

A>Title: Amino acid and cDNA sequences of a vascular endothelial cell mitogen that is

A:Reference number: A35987; MUID:90207249; PMID:2320579  
A:Accession: A35987  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-190 <CON>  
A:Cross-references: GB:M32167; NID:g204287; PIDN:AAA1211.1; PID:g204288

Query Match 85.9%; Score 680.5; DB 2; Length 190;  
Best Local Similarity 87.1%; Pred. No. 1.5e-61;  
Matches 122; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 MNFLLSWHSLALLYLHAKVQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 1 MNFLLSWHWTALLYLHAKVQAAPTTE-GEOKAHEVVKFMDVYQSYCRPIETLVD 59  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 61 IFQEYDPEIYIFKPSVPLMRCGCCNDGECVPTESNITMQIMRIKPHQGHIGEM 120  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 60 IFQEYDPEIYIFKPSVPLMRCGCCNDGECVPTESNITMQIMRIKPHQGHIGEM 119  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 121 SFLOHKNKCECRPKKDRARQK 140  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 120 SFLOHNRCECRPKKDRKPE 139  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8  
A33787  
vascular endothelial growth factor (version 1) - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 16-Mar-1990 #sequence\_revision 16-Mar-1990 #text\_change 05-Nov-1999  
C:Accession: A33787  
R:Rischer, E.; Gospodarowicz, D.; Mitchell, R.; Silva, M.; Schilling, J.; Lau, K.; Crisp  
Biochem. Biophys. Res. Commun. 165, 1198-1206, 1989  
A:Title: Vascular endothelial growth factor: a new member of the platelet-derived growth  
A:Reference number: A33787; MUID:90121225; PMID:2610687  
A:Accession: A33787  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-120 <TIS>  
A:Cross-references: GB:M33750; NID:g163810; PIDN:AAA30805.1; PID:g163811  
C:Keywords: alternative splicing

Query Match 72.7%; Score 575.5; DB 2; Length 120;  
Best Local Similarity 91.3%; Pred. No. 4e-51;  
Matches 105; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 27 APMAEGGQNHHEVVKFMDVYQSYCHPIETLVDIFQEYDPEIYIFKPSVPLMRCGCC 86  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 1 APMAE-GGQKPEHVVKFMDVYQSYCHPIETLVDIFQEYDPEIYIFKPSVPLMRCGCC 59  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 87 CNDEGLECVPTESNITMQIMRIKPHQGHIGEMSFLOHKNKCECRPKKDRARQK 141  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 60 CNDEGLECVPTESNITMQIMRIKPHQGHIGEMSFLOHKNKCECRPKKDRARQK 114  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9  
I51295  
vascular endothelial growth factor - quail (fragment)  
C:Species: Phasianidae gen. sp. (quail)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 28-Feb-1997  
C:Accession: I51295  
R:Flamme, I.; Breier, G.; Risau, W.  
Dev. Biol. 169, 699-712, 1995  
A:Title: Vascular endothelial growth factor (VEGF) and VEGF receptor 2 (flk-1) are expre  
A:Reference number: I51295; MUID:95301109; PMID:7781909  
A:Accession: I51295  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-128 <FLA>  
A:Cross-references: GB:S78343; NID:g999147; PID:g999148  
C:Genetics:  
A:Gene: VEGF

Query Match 46.4%; Score 367.5; DB 2; Length 128;

Best Local Similarity 75.9%; Pred. No. 5.2e-30;  
Matches 63; Conservative 9; Mismatches 10; Indels 1; Gaps 1;  
QY 60 DIFQEYDPEIYIFKPSVPLMRCGCCNDGECVPTESNITMQIMRIKPHQGHIG 119  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 1 DIFQEYDPEIYIFRPSVPLMRCAGCGDEGLECVFVDVYNTMETARIKPHQSHIAH 60  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 120 MSFLOHKNKCECRPKKDRARQK 141  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 61 MSFLOHNSKDCRCPKDKVKNKQK 83  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 10  
A41236  
placental growth factor precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 05-Nov-1999  
C:Accession: A41236  
R:Maglione, D.; Guerriero, V.; Viglietto, G.; Delli-Bovi, P.; Persico, M.G.  
Proc. Natl. Acad. Sci. U.S.A. 88, 9267-9271, 1991  
A:Title: Isolation of a human placenta cDNA coding for a protein related to the vascu  
A:Reference number: A41236; MUID:92021031; PMID:1924389  
A:Accession: A41236  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-149 <MAG>  
A:Cross-references: GB:X54936; NID:g35521; PIDN:CAA38698.1; PID:g35522  
C:Genetics:  
A:Gene: GDB:PGF  
A:Cross-references: GDB:I34676; OMIM:601121  
A:Map position: 14q24-14q31

Query Match 41.0%; Score 325; DB 2; Length 149;  
Best Local Similarity 45.8%; Pred. No. 1.2e-25;  
Matches 55; Conservative 26; Mismatches 35; Indels 4; Gaps 1;

QY 22 KWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVDIFQEYDPEIYIFKPSVPLM 81  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 26 QWALSA----GNSSSEVVVVFQEVWGRSYCRALERLVDVWSEYSPSEVEHMFSPSCVLL 81  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 82 RGGCCNDGECVPTESNITMQIMRIKPHQGHIGEMSFLOHKNKCECRPKKDRARQK 141  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 82 RCTGCGGDNELHCVFETANVTMQLKIRSGDRPSVELTFSQHVRCERCPUREKMKPER 141  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 11  
A56125  
placental growth factor precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 05-Nov-1999  
C:Accession: A56125  
R:DiSalvo, J.; Bayne, M.L.; Conn, G.; Kwok, P.W.; Trivedi, P.G.; Soderman, D.D.; Pal  
J. Biol. Chem. 270, 7717-7723, 1995  
A:Title: Purification and characterization of a naturally occurring vascular endothel  
A:Reference number: A56125; MUID:95221439; PMID:7706320  
A:Accession: A56125  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-158 <DIS>  
A:Cross-references: GB:L40030; NID:g1263413; PIDN:AAA97426.1; PID:g1263414  
C:Keywords: glycoprotein

Query Match 37.1%; Score 294; DB 2; Length 158;  
Best Local Similarity 48.7%; Pred. No. 1.8e-22;  
Matches 58; Conservative 19; Mismatches 40; Indels 2; Gaps 2;

QY 24 SQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVDIFQEYDPEIYIFKPSVPLMRC 83  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 21 SQGA-LSAGNNSTEMEVVFNWGRSYCRPMKELVYIADEHPNEVSHIFSPCVLLSRC 79  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 84 GCGCCNDGECVPTESNITMQIMRIKPHQGH-IGEMSFLOHKNKCECRPKKDRARQK 141  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
DB 80 SGCCGDEGLHCVALKTANTITMQLKIPPNRDPHSYVEMTFSDVLCCECRPILETTKAER 138  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```
RESULT 12
JC4680
vascular endothelial growth factor-related factor 167 precursor - mouse
N:Alternate names: VRP 167 protein
C:Species: Mus musculus (house mouse)
C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 05-Nov-1999
C:Accession: JC4680
R:Townson, S.; Lagercrantz, J.; Grimmond, S.; Sillins, G.; Nordenskjold, M.; Weber, G.;
Biochem. Biophys. Res. Commun. 220, 922-928, 1996
A:Title: Characterization of the murine VEGF-related factor gene.
A:Reference number: JC4679; MUID:96183052; PMID:8607868
A:Accession: JC4680
A:Molecule type: mRNA
A:Residues: 1-188 <TOW>
A:Cross-references: GB:U43837; NID:g1314335; PIDN:AAC52553.1; PID:g1314336
C:Comment: This factor is a mitogen, that is selective for endothelial cells, and belongs
ar endothelial growth factors 167 and VEGF 186.
C:Genetics:
A:Gene: vrf
A:Map position: 19
A:Introns: 137/2
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-188/Product: vascular endothelial growth factor-related factor #status predicted <M>

Query Match 33.3%; Score 264; DB 2; Length 188;
Best Local Similarity 42.7%; Pred. No. 2.4e-19;
Matches 53; Conservative 23; Mismatches 42; Indels 6; Gaps 3;

Qy 12 LALLYLHAKWSQAAPMAEGGQNH-EVVKFMDVQYRSYCHPTIETLVDFIQEYVPDRIE 70
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 10 LVALLQLARTQ----APVQDFGSPSHQKVVVPWIDVYARATCQPREVVVPLSMELMGNV 65

Qy 71 YIFKPSVPLMRGCGCCNDGEGLECVPTESNTITQIMRIKPHOGHIGEMSFLOHKNKEC 130
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 66 KQLVPSCVTVQRCGCCPDGEGLECVPTGQHQVQMILMIQ-YPSSQLGEMSLSEHSQCEC 124

Qy 131 RPKK 134
| | | | |
Db 125 RPKK 128

RESULT 13
JC4679
vascular endothelial growth factor-related factor 186 precursor - mouse
N:Alternate names: VRP 186 protein, VEGF 186
C:Species: Mus musculus (house mouse)
C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 05-Nov-1999
C:Accession: JC4679
R:Townson, S.; Lagercrantz, J.; Grimmond, S.; Sillins, G.; Nordenskjold, M.; Weber, G.;
Biochem. Biophys. Res. Commun. 220, 922-928, 1996
A:Title: Characterization of the murine VEGF-related factor gene.
A:Reference number: JC4679; MUID:96183052; PMID:8607868
A:Accession: JC4679
A:Molecule type: mRNA
A:Residues: 1-207 <TOW>
A:Cross-references: GB:U43836; NID:g1703480; PIDN:AAC52932.1; PID:g1314334
C:Comment: This factor is a mitogen, that is selective for endothelial cells, and belongs
lar endothelial growth factors 167 and 186.
C:Genetics:
A:Gene: vrf
A:Map position: 19
A:Keywords: growth factor
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-207/Product: vascular endothelial growth factor related factor #status predicted <M>

Query Match 33.3%; Score 264; DB 2; Length 207;
Best Local Similarity 42.7%; Pred. No. 2.6e-19;
Matches 53; Conservative 23; Mismatches 42; Indels 6; Gaps 3;

Qy 12 LALLYLHAKWSQAAPMAEGGQNH-EVVKFMDVQYRSYCHPTIETLVDFIQEYVPDRIE 70
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
```

```
Db 10 LVALLQLARTQ----APVQDFGSPSHQKVVVPWIDVYARATCQPREVVVPLSMELMGNV 65
Qy 71 YIFKPSVPLMRGCGCCNDGEGLECVPTESNTITQIMRIKPHOGHIGEMSFLOHKNKEC 130
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 66 KQLVPSCVTVQRCGCCPDGEGLECVPTGQHQVQMILMIQ-YPSSQLGEMSLSEHSQCEC 124

Qy 131 RPKK 134
| | | | |
Db 125 RPKK 128

RESULT 14
B49530
vascular endothelial growth factor homolog A2R, 14.7K - Orf virus
C:Species: Orf virus
C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: B49530
R:Lytile, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.
J. Virol. 68, 84-92, 1994
A:Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus o
A:Reference number: A49530; MUID:94076465; PMID:8254780
A:Contents: NZ2
A:Accession: B49530
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <LYT>
A:Cross-references: GB:S67520; NID:g456897; PIDN:AAB29220.1; PID:g456899
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:141420, NCBIP:141425)

Query Match 29.9%; Score 237; DB 2; Length 133;
Best Local Similarity 44.9%; Pred. No. 9e-17;
Matches 40; Conservative 17; Mismatches 32; Indels 0; Gaps 0;

Qy 45 DVYQSYCHPTIETLVDFIQEYVPDEIEYFKPSCVPLMRGCGCCNDGEGLECVPTESNTITM 104
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 29 EVLKGSECKRPPIVVPVSETHPELTQSRFPNPPCVTLMRCGCCNDGEGLECVPTESNTITM 88
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 105 QIMRIKPHOGHIGEMSFLOHKNKECRPK 133
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 89 ELLGASGSGSNGMORLSFVEHKKCDRPR 117

RESULT 15
S69207
vascular endothelial growth factor C precursor - human
N:Alternate names: FLT4 ligand DHM
C:Species: Homo sapiens (man)
C>Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 08-Oct-1999
C:Accession: S69207; S61795; S71443; S69208; G02659
R:Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukkk, E.; Saksel
EMBO J. 15, 1751, 1996
A:Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand
A:Reference number: S69207; MUID:96203094; PMID:8612600
A:Accession: S69207
A>Status: nucleic acid sequence not shown
A:Residues: 1-419 <JOU>
A:Cross-references: EMBL:X94216; NID:g1177488; PIDN:CAA63907.1; PID:e221096; PID:g118
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A:Note: only a part of the translation is shown
R:Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukkk, E.; Saksel
EMBO J. 15, 290-298, 1996
A:Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4
A:Reference number: S61795; MUID:96178224; PMID:8617204
A:Accession: S61795
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 70-419 <JOU>
A:Note: this sequence has been revised in reference S69207
A:Accession: S71443
A:Molecule type: protein
```

Search completed: November 20, 2002, 05:00:28  
Job time : 51 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 20, 2002, 03:30:52 ; Search time 28 Seconds  
(without alignments)  
208.863 Million cell updates/sec

Title: US-09-884-050-2

Perfect score: 792

Sequence: 1 MNFLSWVHWSLALLYLH.....FLQHNKCEPKKDRARQEK 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	792	100.0	232	1 VEGA_HUMAN	P15692 homo sapien
2	733.5	92.6	190	1 VEGA_PIG	P49151 sus scrofa
3	728.5	92.0	214	1 VEGA_CANFA	Q9myv3 canis famil
4	719.5	90.8	146	1 VEGA_SHEEP	P50412 ovis aries
5	717.5	90.6	190	1 VEGA_BOVIN	P15691 bos taurus
6	708.5	89.5	190	1 VEGA_HORSE	Q9gkr0 equus cabal
7	686.5	86.7	214	1 VEGA_MOUSE	Q00731 mus musculu
8	685.5	86.6	214	1 VEGA_RAT	P16612 rattus norv
9	665.5	84.0	190	1 VEGA_MESAU	Q99ps1 mesocricetu
10	555.5	70.1	216	1 VEGA_CHICK	P52582 gallus gall
11	543.5	68.6	164	1 VEGA_CAVPO	P26617 cavia porce
12	320	40.4	149	1 PLGF_BOVIN	Q9xs47 bos taurus
13	314	39.6	158	1 PLGF_MOUSE	P49764 mus musculu
14	308	38.9	221	1 PLGF_HUMAN	P49763 homo sapien
15	294	37.1	158	1 PLGF_RAT	Q63434 rattus norv
16	267.5	33.8	207	1 VEGB_BOVIN	Q9xs49 bos taurus
17	265.5	33.5	207	1 VEGB_HUMAN	P49765 homo sapien
18	264	33.3	207	1 VEGB_MOUSE	P49766 mus musculu
19	240.5	30.4	135	1 VEGB_RAT	O35485 rattus norv
20	233	29.4	133	1 VEGB_ORFN2	P52584 orf virus (
21	192	24.2	419	1 VEGC_HUMAN	P49767 homo sapien
22	184.5	23.3	415	1 VEGC_MOUSE	P97953 mus musculu
23	172.5	21.8	358	1 VEGD_MOUSE	P97946 mus musculu
24	169.5	21.4	354	1 VEGD_HUMAN	O43915 homo sapien
25	166.5	21.0	326	1 VEGD_RAT	O35251 rattus norv
26	163	20.6	148	1 VEGD_ORFN7	P52585 orf virus (
27	122	15.4	126	1 VEGC_RAT	O35757 rattus norv
28	110.5	14.0	241	1 PGCB_SHEEP	Q95229 ovis aries
29	99.5	12.6	226	1 TSFS_SMSAV	P01128 simian sarc
30	99.5	12.6	241	1 PGCB_HUMAN	P01127 homo sapien
31	99.5	12.6	245	1 PGCB_FELCA	P12919 felis silve
32	96.5	12.2	226	1 PDGA_XENLA	P13698 xenopus lae
33	95	12.0	211	1 PDGA_HUMAN	P04085 homo sapien

## RESULT 1

ID	VEGA_HUMAN	STANDARD;	PRT;	232 AA.
AC	P15692; Q16889; Q60720; Q75875; Q9UL23; Q9UH58; Q9H1W9; Q9H1W8; Q96NW5;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).			
DE	VEGF OR VEGFA.			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM VEGF189 AND VEGF165).			
RX	MEDLINE=90069608; PubMed=2479986;			
RA	Leung D.W., Cachianes G., Kuang W.-J., Goeddel D.V., Ferrara N.;			
RT	"Vascular endothelial growth factor is a secreted angiogenic mitogen.";			
RT	Science 246:1306-1309(1989).			
RL	[2]			
RN	SEQUENCE FROM N.A. (ISOFORM VEGF189), AND PARTIAL SEQUENCE.			
RX	MEDLINE=90069609; PubMed=2479987;			
RA	Keck P.J., Hauser S.D., Krivi G., Sanzo K., Warren T., Feder J., Connolly D.T.;			
RT	"Vascular permeability factor, an endothelial cell mitogen related to PDGF.";			
RT	Science 246:1309-1312(1989).			
RL	[3]			
RN	SEQUENCE FROM N.A. (ISOFORM VEGF189).			
RP	MEDLINE=91268072; PubMed=1711045;			
RX	Tischer E., Mitchell R., Hartman T., Silva M., Gospodarowicz D., Fiddes J.C., Abraham J.A.;			
RT	"The human gene for vascular endothelial growth factor. Multiple protein forms are encoded through alternative exon splicing.";			
RT	J. Biol. Chem. 266:11947-11954(1991).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM VEGF206).			
RX	MEDLINE=92168017; PubMed=1791831;			
RA	Houck K.A., Ferrara N., Winer J., Cachianes G., Li B., Leung D.W.;			
RT	"The vascular endothelial growth factor family: identification of a fourth molecular species and characterization of alternative splicing of RNA.";			
RT	Mol. Endocrinol. 5:1806-1814(1991).			
RL	[5]			
RN	SEQUENCE FROM N.A. (ISOFORM VEGF165).			
RP	MEDLINE=92231879; PubMed=1567395;			
RX	Weindel K., Marne D., Weich H.A.;			
RT	"AIDS-associated Kaposi's sarcoma cells in culture express vascular endothelial growth factor.";			
RT	Biochem. Biophys. Res. Commun. 183:1167-1174(1992).			
RL	[6]			
RN	SEQUENCE FROM N.A. (ISOFORM VEGF145).			
RP	MEDLINE=97207275; PubMed=9054410;			

34	94.5	11.9	204	1	PDGA_RAT	P28576 rattus norv
35	94.5	11.9	211	1	PDGA_MOUSE	P20033 mus musculu
36	94.5	11.9	213	1	PDGA_RABIT	P34007 oryctolagus
37	93	11.7	241	1	PDGB_MOUSE	P31240 mus musculu
38	92	11.6	225	1	PDGB_RAT	Q05028 rattus norv
39	89	11.2	28	1	ICPP_VIPLE	P82475 vipera lebe
40	81.5	10.3	2499	1	MPRI_BOVIN	P08169 bos taurus
41	80	10.1	799	1	ITBN_DROME	Q27591 drosophila
42	74.5	9.4	471	1	MM13_RABIT	O62806 oryctolagus
43	74	9.3	354	1	VANA_PSESP	O05616 pseudomonas
44	74	9.3	466	1	MM13_RAT	P23097 rattus norv
45	73	9.2	406	1	YMX2_CAEEL	P34510 caenorhabdi

## ALIGNMENTS

RA Poltorak Z., Cohen T., Sivan R., Kandelis Y., Spira G., Vlodevsky I.,  
 RA Keshet E., Neufeld G.;  
 RT "VEGF145, a secreted vascular endothelial growth factor isoform that  
 RT binds to extracellular matrix.";  
 RL J. Biol. Chem. 272:7151-7158(1997).  
 [7]  
 RN SEQUENCE FROM N.A. (ISOFORM VEGF183).  
 RP TISSUE-Kidney;  
 RC MEDLINE-99096474; PubMed-9878851;  
 RX Lei J., Jiang A., Pei D.;  
 RA "Identification and characterization of a new splicing variant of  
 RT vascular endothelial growth factor: VEGF183.";  
 RL Biochim. Biophys. Acta 1443:400-406(1998).  
 [8]  
 RN SEQUENCE FROM N.A. (ISOFORM VEGF165).  
 RP TISSUE-Breast;  
 RC MEDLINE-98119755; PubMed-9450968;  
 RX Claffey K.P., Shih S.-C., Mullen A., Dziennis S., Cusick J.L.,  
 RA Abrams K.R., Lee S.W., Detmar M.;  
 RT "Identification of a human VPF/VEGF 3' untranslated region mediating  
 RT hypoxia-induced mRNA stability.";  
 RL Mol. Biol. Cell 9:469-481(1998).  
 [9]  
 RN SEQUENCE OF 114-209 FROM N.A. (ISOFORM VEGF183).  
 RP TISSUE-Retina;  
 RC MEDLINE-99165303; PubMed-10067980;  
 RX Jingjing L., Xue Y., Agarwal N., Roque R.S.;  
 RA "Human Muller cells express VEGF183, a novel spliced variant of  
 RT vascular endothelial growth factor.";  
 RL Invest. Ophthalmol. Vis. Sci. 40:752-759(1999).  
 [10]  
 RN SEQUENCE FROM N.A. (ISOFORM VEGF165).  
 RP TISSUE-Hemangioblastoma;  
 RC Murata H., Fukushima J., Hattori S., Okuda K., Yanagi H.;  
 RA "Human cDNA for the vascular endothelial growth factor isoform  
 RT VEGF165.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 [11]  
 RN SEQUENCE FROM N.A. (ISOFORM VEGF148).  
 RP TISSUE-Renal glomerulus;  
 RC MEDLINE-99394945; PubMed-10464055;  
 RX Whittle C.J., Gillespie K.M., Harrison R., Mathieson P.W.,  
 RA Harper S.J.;  
 RT "Heterogeneous vascular endothelial growth factor (VEGF) isoform mRNA  
 RT and receptor mRNA expression in human glomeruli, and the  
 RL identification of VEGF148 mRNA, a novel truncated splice variant.";  
 RL Clin. Sci. 97:303-312(1999).  
 [12]  
 RN SEQUENCE FROM N.A. (ISOFORM VEGF121).  
 RP Sato J.D., Whitney R.G.;  
 RA "Human cDNA for vascular endothelial growth factor isoform VEGF121.";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 [13]  
 RN SEQUENCE FROM N.A.  
 RP Williams S.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 [14]  
 RN SEQUENCE OF 23-232 FROM N.A. (VEGF165).  
 RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,  
 RA Peel C.L., Toth E.J., Yi O., Nickerson D.A.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 [15]  
 RN PRELIMINARY SEQUENCE OF 27-36; 43-50 AND 59-81.  
 RX MEDLINE-90062112; PubMed-2584205;  
 RA Connolly D.T., Olander J.V., Heuvelman D., Nelson R., Monsell R.,  
 RA Siegel N., Haymore B.L., Leimgruber R., Feder J.;  
 RT "Human vascular permeability factor. Isolation from U937 cells.";  
 RL J. Biol. Chem. 264:20017-20024(1989).  
 [16]  
 RN SEQUENCE OF 27-41.  
 RX MEDLINE-93145946; PubMed-7678805;  
 RA Fiebig B.L., Jaeger B., Schoellmann C., Weindel K., Wilting J.,  
 RA Kochs G., Marne D., Hug H., Welch H.A.;

RT "Synthesis and assembly of functionally active human vascular  
 RT endothelial growth factor homodimers in insect cells.";  
 RL Eur. J. Biochem. 211:19-26(1993).  
 [17]  
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 34-135.  
 RP MEDLINE-97352774; PubMed-9207067;  
 RX Muller Y.A., Li B., Christinger H.W., Wells J.A., Cunningham B.C.,  
 RA de Vos A.M.;  
 RT "Vascular endothelial growth factor: crystal structure and functional  
 RT mapping of the kinase domain receptor binding site.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:7192-7197(1997).  
 [18]  
 RN X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS) OF 34-135.  
 RP MEDLINE-98035455; PubMed-9351807;  
 RX Muller Y.A., Christinger H.W., Keyt B.A., de Vos A.M.;  
 RA "The crystal structure of vascular endothelial growth factor (VEGF)  
 RT refined to 1.93-A resolution: multiple copy flexibility and receptor  
 RT binding.";  
 RL Structure 5:1325-1338(1997).  
 [19]  
 RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 39-134.  
 RP MEDLINE-99119204; PubMed-9922142;  
 RX Wiesmann C., Christinger H.W., Cochran A.G., Cunningham B.C.,  
 RA Fairbrother W.J., Keenan C.J., Meng G., de Vos A.M.;  
 RT "Crystal structure of the complex between VEGF and a receptor-blocking  
 RT peptide.";  
 RL Biochemistry 37:17765-17772(1998).  
 [20]  
 RN STRUCTURE BY NMR OF 34-135.  
 RP MEDLINE-97477915; PubMed-9336848;  
 RX Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,  
 RA Starovasnik M.A.;  
 RT "1H, 13C, and 15N backbone assignment and secondary structure of the  
 RL receptor-binding domain of vascular endothelial growth factor.";  
 RL Protein Sci. 6:2250-2260(1997).  
 [21]  
 RN STRUCTURE BY NMR OF 137-215.  
 RP MEDLINE-98298440; PubMed-9634701;  
 RX Fairbrother W.J., Champe M.A., Christinger H.W., Keyt B.A.,  
 RA Starovasnik M.A.;  
 RT "Solution structure of the heparin-binding domain of vascular  
 RL endothelial growth factor.";  
 RL Structure 6:637-648(1998).  
 [22]  
 RN FUNCTION.  
 RP MEDLINE-21320570; PubMed-11427521;  
 RX Murphy J.F., Fitzgerald D.J.;  
 RA "Vascular endothelial growth factor induces cyclooxygenase-dependent  
 RT proliferation of endothelial cells via the VEGF-2 receptor.";  
 RL FASEB J. 15:1667-1669(2001).  
 CC -1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and  
 CC endothelial cell growth. It induces endothelial cell  
 CC proliferation, promotes cell migration, inhibits apoptosis, and  
 CC induces permeabilization of blood vessels. It binds to the  
 CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and  
 CC heparin. Neuropilin-1 binds isoforms VEGF-165 and VEGF-145.  
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer  
 CC with PlGF (By similarity).  
 CC -1- SUBCELLULAR LOCATION: VEGF121 is acidic and freely secreted.  
 CC VEGF165 is more basic, has heparin-binding properties and,  
 CC although a significant proportion remains cell-associated, most is  
 CC freely secreted. VEGF189 is very basic; it is cell-associated  
 CC after secretion and is bound avidly by heparin and the  
 CC extracellular matrix, although it may be released as a soluble  
 CC form by heparin, heparinase or plasmin.  
 CC -1- ALTERNATIVE PRODUCTS: 7 isoforms: VEGF206 (shown here), VEGF189,  
 CC VEGF183, VEGF165/VEGF, VEGF148, VEGF145 and VEGF121; may be  
 CC produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: The VEGF189, VEGF-165 and VEGF-121 isoforms  
 CC are widely expressed, whereas the VEGF206 and VEGF-145 are  
 CC uncommon.  
 CC -1- INDUCTION: Regulated by growth factors, cytokines, gonadotropins,  
 CC nitric oxide, hypoxia, hypoglycemia and oncogenic mutations.



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Query Match      100.0%; Score 792; DB 1; Length 232;
Best Local Similarity 100.0%; Pred. No. 5e-76;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYORSYCHPITETLVD 60
DB 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYORSYCHPITETLVD 60

QY 61 IFQEPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHOGHIGEM 120
DB 61 IFQEPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHOGHIGEM 120

QY 121 SFLQHNKCECRPKDRARQEK 141
DB 121 SFLQHNKCECRPKDRARQEK 141

RESULT 2
VEGA_PIG
ID VEGA_PIG STANDARD; PRT; 190 AA.
AC P49151; Q9GL52;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).
GN VEGF OR VEGFA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95143284; PubMed=7841203;
RA Sharma H.S., Tang Z.H., Gho B.C.H., Verdouw P.D.;
RT "Nucleotide sequence and expression of the porcine vascular endothelial growth factor.";
RL Biochim. Biophys. Acta 1260:235-238(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Lee T., Canty J.M.;
RT "PCR cloning of porcine cardiac vascular endothelial growth factor gene.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the VEGFR1/Fit-1 and VEGFR2/Kdr receptors and to heparan sulfate and heparin (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PlGF (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By similarity).
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC -----
DR EMBL; X81380; CAA57143.1; -
DR EMBL; AF318502; AAG33064.1; -
DR HSSP; PL5692; 1VGH.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
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DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 190
FT DISULFID 51 93
FT DISULFID 82 127
FT DISULFID 86 129
FT DISULFID 76 76
FT DISULFID 85 85
FT CARBOHYD 100 100
FT CONFLICT 102 102
SQ SEQUENCE 190 AA; 22368 MW; 04D40B8D7913047F CRC64;

Query Match      92.6%; Score 733.5; DB 1; Length 190;
Best Local Similarity 95.7%; Pred. No. 5.6e-70;
Matches 134; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1 MNFLSWHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYORSYCHPITETLVD 60
DB 1 MNFLSWHWSLALLYLHAKWSQAAPMAE-GDQKPEVVKFMDVYORSYCRPIETLVD 59

QY 61 IFQEPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHOGHIGEM 120
DB 61 IFQEPDEIEYIFKPCVPLMRCGCCNDEGLECVPTESNITMIMRIKPHOGHIGEM 119

QY 121 SFLQHNKCECRPKDRARQEK 140
DB 120 SFLQHNKCECRPKDRARQEK 139

RESULT 3
VEGA_CANFA
ID VEGA_CANFA STANDARD; PRT; 214 AA.
AC Q9MYV3; Q9XSF5; Q9XSF4; Q9XSF3;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).
GN VEGF OR VEGFA.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM VEGF188).
RX MEDLINE=20125516; PubMed=10661874;
RA Scheidegger P., Weighhofer W., Suarez S., Kaser-Hotz B., Steiner R., Ballmer-Hofer K., Jaussel R.;
RT "Vascular endothelial growth factor (VEGF) and its receptors in tumor-bearing dogs.";
RL Biol. Chem. 380:1449-1454(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS VEGF188; VEGF-182 AND VEGF-164).
RC TISSUE=Heart;
RA Jingjing L., Roque R.S.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the VEGFR1/Fit-1 and VEGFR2/Kdr receptors and to heparan sulfate and heparin (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PlGF (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or to the extracellular matrix unless released by heparin (By similarity).
CC -!- ALTERNATIVE PRODUCTS: At least 3 isoforms; VEGF188 (shown here), VEGF182 and VEGF164; are produced by alternative splicing.
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CC      -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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CC      -----
DR      EMBL: AJ133758; CAB82426.1; -
DR      EMBL: AF133250; RAD29684.1; -
DR      EMBL: AF133249; RAD29683.1; -
DR      EMBL: AF133248; RAD29682.1; -
DR      HSSP: P15692; LVGH.
DR      InterPro: IPR000072; PD_growth_factor.
DR      ProDom: PD001629; PD_growth_factor; 1.
DR      SMART: SM00141; PDGF_1.
DR      PROSITE: PS00249; PDGF_1; 1.
DR      PROSITE: PS0278; PDGF_2; 1.
KW      Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW      Heparin-binding; Alternative splicing; Multigene family.
FT      SIGNAL 1 26
FT      CHAIN 27 214
FT      DISULFID 51 93
FT      DISULFID 82 127
FT      DISULFID 86 129
FT      DISULFID 76 76
FT      DISULFID 85 85
FT      CARBOHYD 100 100
FT      VARSPLIC 140 140
FT      VARSPLIC 141 164
FT      VARSPLIC 159 164
FT      CONFLICT 143 143
FT      CONFLICT 161 161
FT      SEQUENCE 214 AA; 25175 MW; 0AC980A158C44B27 CRC64;
Query Match 92.0%; Score 728.5; DB 1; Length 214;
Best Local Similarity 94.3%; Pred. No. 2.1e-69;
Matches 133; Conservative 1; Mismatches 6; Indels 1; Gaps 1;
QY      1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60
DB      1 MNFLSWVHWSLALLYLHAKWSQAAPMA-GGEHKPHEVVKFMDVYQSYCHPIETLVD 59
QY      61 IFQEYPDETEYIFKPCVPLMRGCGCCNDEGLECVPTESNITMQLMRKPHOGQHIGEM 120
DB      60 IFQEYPDETEYIFKPCVPLMRGCGCCNDEGLECVPTESNITMQLMRKPHOGQHIGEM 119
QY      121 SFLQHNKCECRPKKDRARQEK 141
DB      120 SFLQHSKCECRPKKDRARQEK 140
RESULT 4
VEGA_SHEEP
ID      VEGA_SHEEP STANDARD; PRT; 146 AA.
AC      P50412;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DE      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE      permeability factor) (VPF).
GN      VEGF OR VEGFA.
OS      Ovis aries (Sheep).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Caprinae; Ovis.
OX      NCBI_TaxID=9940;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-Kidney;

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RX      MEDLINE-971117958; PubMed-8958842;
RA      Redmer D.A., Dai Y., Li J., Charnock-Jones D.S., Smith S.K.,
RA      Reynolds L.P., Moor R.M.;
RT      "Characterization and expression of vascular endothelial growth
RT      factor (VEGF) in the ovine corpus luteum.";
RL      J. Reprod. Fertil. 108:157-165(1996).
CC      -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC      endothelial cell growth. It induces endothelial cell
CC      proliferation, promotes cell migration, inhibits apoptosis, and
CC      induces permeabilization of blood vessels. It binds to the
CC      VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC      heparin (by similarity).
CC      -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC      with PLGF (by similarity).
CC      -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X89506; CAA61677.1; -
DR      HSSP: P15692; LVPP.
DR      InterPro: IPR000072; PD_growth_factor.
DR      Pfam: PF00341; PDGF_1.
DR      ProDom: PD001629; PD_growth_factor; 1.
DR      SMART: SM00141; PDGF_1.
DR      PROSITE: PS00249; PDGF_1; 1.
DR      PROSITE: PS0278; PDGF_2; 1.
KW      Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW      Heparin-binding; Multigene family.
FT      SIGNAL 1 26
FT      CHAIN 27 146
FT      DISULFID 51 93
FT      DISULFID 82 127
FT      DISULFID 86 129
FT      DISULFID 76 76
FT      DISULFID 85 85
FT      CARBOHYD 100 100
FT      SEQUENCE 146 AA; 17247 MW; 4E792CB557F91760 CRC64;
Query Match 90.8%; Score 719.5; DB 1; Length 146;
Best Local Similarity 92.2%; Pred. No. 1.2e-68;
Matches 130; Conservative 4; Mismatches 6; Indels 1; Gaps 1;
QY      1 MNFLSWVHWSLALLYLHAKWSQAAPMAEGGGQNHHEVVKFMDVYQSYCHPIETLVD 60
DB      1 MNFLSWVHWSLALLYLHAKWSQAAPMAE-GGOKPHEVVKFMDVYQSYCHPIETLVD 59
QY      61 IFQEYPDETEYIFKPCVPLMRGCGCCNDEGLECVPTESNITMQLMRKPHOGQHIGEM 120
DB      60 IFQEYPDETEYIFKPCVPLMRGCGCCNDEGLECVPTESNITMQLMRKPHOGQHIGEM 119
QY      121 SFLQHNKCECRPKKDRARQEK 141
DB      120 SFLQHNKCECRPKKDRARQEK 140
RESULT 5
VEGA_BOVIN
ID      VEGA_BOVIN STANDARD; PRT; 190 AA.
AC      P15691;
DT      01-APR-1990 (Rel. 14, Created)
DT      01-APR-1990 (Rel. 14, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE      permeability factor) (VPF).
GN      VEGF OR VEGFA.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OX Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.  
 RX MEDLINE=90069608; PubMed=2479986;  
 RA Leung D.W., Cachlanes G., Kuang W.-J., Goeddel D.V., Ferrara N.;  
 RT "Vascular endothelial growth factor is a secreted angiogenic  
 RT mitogen.";  
 RL Science 246:1306-1309(1989).  
 [2]  
 RP SEQUENCE OF 27-190 FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RX MEDLINE=90121225; PubMed=2610687;  
 RA Tischer E., Gospodarowicz D., Mitchell R., Silva M., Schilling J.,  
 RA Lau K., Crisp T., Fiddes J.C., Abraham J.A.;  
 RT "Vascular endothelial growth factor: a new member of the platelet-  
 RT derived growth factor gene family.";  
 RL Biochem. Biophys. Res. Commun. 165:1198-1206(1989).  
 [3]  
 RP SEQUENCE OF 27-31.  
 RX MEDLINE=89286596; PubMed=2735925;  
 RA Ferrara N., Henzel W.J.;  
 RT "pituitary follicular cells secrete a novel heparin-binding growth  
 RT factor specific for vascular endothelial cells.";  
 RL Biochem. Biophys. Res. Commun. 161:851-858(1989).  
 CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and  
 CC endothelial cell growth. It induces endothelial cell  
 CC proliferation, promotes cell migration, inhibits apoptosis, and  
 CC induces permeabilization of blood vessels. It binds to the  
 CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and  
 CC heparin (By similarity).  
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer  
 CC with PLGF (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or  
 CC to the extracellular matrix unless released by heparin (By  
 CC similarity).  
 CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta; are  
 CC produced by alternative splicing.  
 CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M32976; AAA30502.1; -;  
 CC EMBL; M31836; AAA30804.1; -;  
 CC EMBL; M33750; AAA30805.1; -;  
 CC PIR; A33255; A33255.  
 CC PIR; A33787; A33787.  
 CC PIR; B40080; B40080.  
 CC HSP; P15692; IVGH.  
 CC InterPro; IPR000072; PD\_growth\_factor.  
 CC Pfam; PF00341; PDGF; 1.  
 CC ProDom; PD001629; PD\_growth\_factor; 1.  
 CC SMART; SM00141; PDGF; 1.  
 CC PROSITE; PS00249; PDGF\_1; 1.  
 CC PROSITE; PS50278; PDGF\_2; 1.  
 CC Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;  
 KW Heparin-binding; Alternative splicing; Multigene family.  
 FT SIGNAL 1 26  
 FT CHAIN 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR A.  
 FT DISULFID 51 93 BY SIMILARITY.  
 FT DISULFID 82 127 BY SIMILARITY.  
 FT DISULFID 86 129 BY SIMILARITY.  
 FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 100 100 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT VARSPPLIC 139 183 MISSING (IN ISOFORM BETA).  
 FT VARSPPLIC 184 184 R -> K (IN ISOFORM BETA).

SQ SEQUENCE 190 AA; 22310 MW; EDBF903E46E24789 CRC64;  
 Query Match 90.6%; Score 717.5; DB 1; Length 190;  
 Best Local Similarity 92.9%; Pred. No. 2.7e-68;  
 Matches 130; Conservative 3; Mismatches 6; Indels 1; Gaps 1;  
 QY 1 MNFLLSWVHNSLALLYLHHAQKWSQAAPMAEGGQNHHEVVKFMDVYQRSYCHPIETLVD 60  
 Db 1 MNFLLSWVHNSLALLYLHHAQKWSQAAPMAE-GGQKPEVVKFMDVYQRSFCHPIETLVD 59  
 QY 61 IQEYYPDEIEYIFKPCVPLMRCGGCCNDEGLECYPTESNITMQIMRKPHQGHIGEM 120  
 Db 60 IQEYYPDEIEYIFKPCVPLMRCGGCCNDEGLECYPTESNITMQIMRKPHQGHIGEM 119  
 QY 121 SFLQHNKCECRPKDKAROE 140  
 Db 120 SFLQHNKCECRPKDKAROE 139  
 RESULT 6  
 VEGA\_HORSE  
 ID VEGA\_HORSE STANDARD; PRT; 190 AA.  
 AC Q9GKR0;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular  
 DE permeability factor) (VPF).  
 GN VEGF OR VEGFA.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Miura N., Misumi K., Kawahara K., Nakashima M., Fukumitsu S.,  
 RA Kawabata H., Uto N., Oka T., Maruyama I., Sakamoto H.;  
 RT "Cloning of cDNA and high-level expression of equine vascular  
 RT endothelial growth factor (VEGF)."  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Growth factor active in angiogenesis, and endothelial  
 CC cell growth. Induces endothelial proliferation and vascular  
 CC permeability (By similarity).  
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer  
 CC with PLGF (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or  
 CC to the extracellular matrix unless released by heparin (By  
 CC similarity).  
 CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AB053350; BAB20890.1; -;  
 CC HSP; P15692; IVGH.  
 CC InterPro; IPR000072; PD\_growth\_factor.  
 CC Pfam; PF00341; PDGF; 1.  
 CC ProDom; PD001629; PD\_growth\_factor; 1.  
 CC SMART; SM00141; PDGF; 1.  
 CC PROSITE; PS00249; PDGF\_1; 1.  
 CC PROSITE; PS50278; PDGF\_2; 1.  
 CC Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;  
 KW Multigene family.  
 FT SIGNAL 1 26  
 FT CHAIN 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR A.  
 FT DISULFID 51 93 BY SIMILARITY.  
 FT DISULFID 82 127 BY SIMILARITY.  
 FT DISULFID 86 129 BY SIMILARITY.

```

FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 190 AA; 22312 MW; 87E9E161439E5F87 CRC64;

Query Match 89.5%; Score 708.5; DB 1; Length 190;
Best Local Similarity 92.1%; Pred. No. 2.4e-67;
Matches 129; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 MNFLLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
DB 1 MNFLLSWVHWSLALLYLHAKWSQAAPMAEGGKHKT-HEVVKFMDVYQSYCHPIETLVD 59
QY 61 IFQEPDEIEYIFKPCVPLMRGCGCNDGECVPTESNITMQIMRKPHQGHIGEM 120
DB 60 IFQEPDEIEYIFKPCVPLMRGCGCNDGECVPTAEFNITMQIMRKPHQSHIGEM 119

QY 121 SFLQHNKCECRPKKDRARQE 140
DB 120 SFLQHSKCECRPKKDRARQE 139

RESULT 7
VEGA_MOUSE STANDARD; PRT; 214 AA.
AC Q00731;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).
GN VEGF OR VEGFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS VEGF-1; VEGF-2 AND VEGF-3).
RX MEDLINE=92274860; PubMed=1592003;
RA Breier G., Albrecht U., Sterrer S., Risau W.;
RT "Expression of vascular endothelial growth factor during embryonic angiogenesis and endothelial cell differentiation.";
RL Development 114:521-532(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM VEGF-1).
RX MEDLINE=92355593; PubMed=1644816;
RA Claffey K.P., Wilkison W.O., Spiegelman B.M.;
RT "Vascular endothelial growth factor. Regulation by cell differentiation and activated second messenger pathways.";
RL J. Biol. Chem. 267:16317-16322(1992).
RN [3]
RP SEQUENCE OF 1-3 FROM N.A.
RX MEDLINE=96216498; PubMed=8632007;
RA Shima D.T., Kuroki M., Deutsch U., Ng Y., Adamis A.P., D'Amore P.A.;
RT "The mouse gene for vascular endothelial growth factor. Genomic structure, definition of the transcriptional unit, and characterization of transcriptional and post-transcriptional regulatory sequences.";
RL J. Biol. Chem. 271:3877-3883(1996).
CC -1- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. It induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis, and induces permeabilization of blood vessels. It binds to the VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and heparin (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer with PlGF (By similarity).
CC -1- SUBCELLULAR LOCATION: VEGF-1 and VEGF-2 are secreted while VEGF-3 remains cell-surface associated unless released by heparin.
CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; VEGF-3/VEGF188 (shown here), VEGF-1/VEGF164 and VEGF-2/VEGF120; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: In developing embryos, expressed mainly in the choroid plexus, paraventricular neuroepithelium, placenta and kidney glomeruli. Also found in bronchial epithelium, adrenal gland and in seminiferous tubules of testis. High expression of VEGF continues in kidney glomeruli and choroid plexus in adults.
CC -1- DOMAIN: VEGF-3 contains a basic insert which acts as a cell retention signal.
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
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CC EMBL: S37052; AAB22252.1; -
CC EMBL: S38083; AAB22253.1; -
CC EMBL: S38100; AAB22254.1; -
CC EMBL: M95200; AAA40547.1; -
CC EMBL: U41383; -; NOT_ANNOTATED_CDS.
CC PIR: A43351; A43351.
CC HSSP: P15692; 2VPF.
CC MGD: MGI:103178; Vegfa.
CC InterPro: IPR000072; PD_growth_factor.
CC Pfam: PF00341; PDGF; 1.
CC ProDom: PD001629; PD_growth_factor; 1.
CC SMART: SM00141; PDGF; 1.
CC PROSITE: PS00249; PDGF_1; 1.
CC PROSITE: PS0278; PDGF_2; 1.
CC Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Alternative splicing; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 214 VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT DISULFID 51 93 BY SIMILARITY.
FT DISULFID 82 127 BY SIMILARITY.
FT DISULFID 86 129 BY SIMILARITY.
FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).
FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (PROBABLE).
FT VARSPLIC 140 140 K -> N (IN ISOFORM VEGF-1).
FT VARSPLIC 141 164 MISSING (IN ISOFORM VEGF-1).
FT VARSPLIC 141 208 MISSING (IN ISOFORM VEGF-2).
FT CONFLICT 117 118 GE -> ER (IN REF. 2).
SQ SEQUENCE 214 AA; 25283 MW; B5540B51E4BB6E17 CRC64;

Query Match 86.7%; Score 686.5; DB 1; Length 214;
Best Local Similarity 87.2%; Pred. No. 5.5e-65;
Matches 123; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 MNFLLSWVHWSLALLYLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
DB 1 MNFLLSWVHWSLALLYLHAKWSQAAPTE-GEQKSHEVVKFMDVYQSYCHPIETLVD 59
QY 61 IFQEPDEIEYIFKPCVPLMRGCGCNDGECVPTESNITMQIMRKPHQGHIGEM 120
DB 60 IFQEPDEIEYIFKPCVPLMRGCGCNDGECVPTESNITMQIMRKPHQSHIGEM 119

QY 121 SFLQHNKCECRPKKDRARQE 141
DB 120 SFLQHSRCECRPKKDRARQE 140

RESULT 8
VEGA_MOUSE STANDARD; PRT; 214 AA.
AC P16612; Q9QXG7; Q9QXG6; Q9JXX7;
DT 01-AUG-1990 (Rel. 15, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF).
GN VEGF OR VEGFA.

```

OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM VEGF-A164), AND SEQUENCE OF 27-190.  
RX MEDLINE=90207249; PubMed=2320579;  
RA Conn G., Bayne M.L., Soderman D.D., Kwok P.W., Sullivan K.A.,  
RA Palisi T.M., Hope D.A., Thomas K.A.;  
RT "Amino acid and cDNA sequences of a vascular endothelial cell mitogen  
RT that is homologous to platelet-derived growth factor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:2628-2633(1990).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS VEGF-A188; VEGF-A164; VEGF-A144 AND  
RP VEGF-A120).  
RA Ishii H., Arakawa T., Okayama M., Oota I., Takuma T., Inomata K.;  
RT "Developmental expression of vascular endothelial growth factor-A  
RT (VEGF-A) splicing variants, VEGF-A188, VEGF-A164, and VEGF-A120 in rat  
RT masseter muscle.";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 27-40.  
RC TISSUE=Glial tumor;  
RX MEDLINE=95221439; PubMed=7706320;  
RA DiSalvo J., Bayne M.L., Conn G., Kwok P.W., Trivedi P.G.,  
RA Soderman D.D., Palisi T.M., Sullivan K.A., Thomas K.A.;  
RT "Purification and characterization of a naturally occurring vascular  
RT endothelial growth factor/placenta growth factor heterodimer.";  
RL J. Biol. Chem. 270:7717-7723(1995).  
CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and  
CC endothelial cell growth. It induces endothelial cell  
CC proliferation, promotes cell migration, inhibits apoptosis, and  
CC induces permeabilization of blood vessels. It binds to the  
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and  
CC heparin (By similarity).  
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer  
CC with pLGF (By similarity).  
CC -!- SUBCELLULAR LOCATION: VEGF-A120 is acidic and freely secreted.  
CC VEGF-A164 is more basic, has heparin-binding properties and,  
CC although a significant proportion remains cell-associated, most is  
CC freely secreted. VEGF-A188 is very basic; it is cell-associated  
CC after secretion and is bound avidly by heparin and the  
CC extracellular matrix, although it may be released as a soluble  
CC form by heparin, heparinase or plasmin (By similarity).  
CC -!- ALTERNATIVE PRODUCTS: At least 4 isoforms: VEGF-A188 (shown here),  
CC VEGF-A164, VEGF-A144 and VEGF-A120; are produced by alternative  
CC splicing.  
CC -!- TISSUE SPECIFICITY: Expressed in the pituitary, in brain, in  
CC particularly in supraoptic and paraventricular nuclei and the  
CC choroid plexus. Also found abundantly in the corpus luteum of  
CC the ovary and in kidney glomeruli.  
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M32167; AAA41211.1; -  
CC EMBL; AF215725; AAF19211.1; -  
CC EMBL; AF215726; AAF19212.1; -  
CC EMBL; AF222779; AAF25958.1; -  
CC PIR; A35987; A35987.  
CC HSSP; P15692; 1VPP.  
CC InterPro; IPR000072; PD\_growth\_factor.  
CC Pfam; PF00341; PDGF; 1  
CC ProDom; PD001629; PD\_growth\_factor; 1.  
CC SMART; SM00141; PDGF; 1.  
CC PROSITE; PS00249; PDGF\_1; 1.  
CC PROSITE; PS0278; PDGF\_2; 1.

KW Mitogen: Angiogenesis; Growth factor; Glycoprotein; Signal;  
KW Heparin-binding; Alternative splicing; Multigene family.  
FT SIGNAL 1 26 VASCULAR ENDOTHELIAL GROWTH FACTOR A.  
FT CHAIN 27 214 BY SIMILARITY.  
FT DISULFID 51 93 BY SIMILARITY.  
FT DISULFID 82 127 BY SIMILARITY.  
FT DISULFID 86 129 BY SIMILARITY.  
FT DISULFID 76 76 INTERCHAIN (BY SIMILARITY).  
FT DISULFID 85 85 INTERCHAIN (BY SIMILARITY).  
FT CARBOHYD 100 100 N-LINKED (GLCNAC...).  
FT VARSPLIC 140 140 K -> N (IN ISOFORM VEGF-A164).  
FT VARSPLIC 141 164 MISSING (IN ISOFORM VEGF-A164).  
FT VARSPLIC 141 208 MISSING (IN ISOFORM VEGF-A120).  
FT VARSPLIC 165 208 MISSING (IN ISOFORM VEGF-A144).  
FT CONFLICT 101 101 V -> A (IN REF. 2; AAF19212).  
SQ SEQUENCE 214 AA; 25239 MW; 60FB876F530496 CRC64;  
  
Query Match 86.6%; Score 685.5; DB 1; Length 214;  
Best Local Similarity 87.2%; Pred. No. 7e-65;  
Matches 123; Conservative 5; Mismatches 12; Indels 1; Gaps 1;  
  
QY 1 MNFLSNVWHSALALLYLHAKWSQAAPMAEGGGQNHHEVYKFMVYORSYCHPIETLVD 60  
Db 1 MNFLSNVWHSALALLYLHAKWSQAAPTE-GEOKAHEVWKFMDVYORSYCRPIETLVD 59  
QY 61 IFQEYPDIEYIFKPSVPLMRGCGCCNDGECVPTESNITMOIMRIKPHQSHIGEM 120  
Db 60 IFQEYPDIEYIFKPSVPLMRGCGCCNDGECVPTESNITMOIMRIKPHQSHIGEM 119  
QY 121 SFLQNKCECPKDKRQREK 141  
Db 120 SFLQHSRCECPKDKRTKPEK 140  
  
RESULT 9  
VEGA\_MESAU STANDARD; PRT; 190 AA.  
AC Q99PS1;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular  
DE permeability factor) (VPF).  
GN VEGF OR VEGFA.  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
OX NCBI\_TaxID=10036;  
RN [1]  
RP SEQUENCE FROM N.A. and Embryo;  
RC TISSUE=Decidua, and Embryo;  
RA Yi X.J., Chow P.H.;  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and  
CC endothelial cell growth. It induces endothelial cell  
CC proliferation, promotes cell migration, inhibits apoptosis, and  
CC induces permeabilization of blood vessels. It binds to the  
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and  
CC heparin (By similarity).  
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer  
CC with pLGF (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted but remains associated to cells or  
CC to the extracellular matrix unless released by heparin (By  
CC similarity).  
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
CC  
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CC  EMBL; AF063013; AAK00049.1; -
DR  HSSP; P15692; 1VGH.
DR  InterPro; IPR000072; PD_growth_factor.
DR  Pfam; PF00341; PDGF; 1.
DR  ProDom; PD001629; PD_growth_factor; 1.
DR  SMART; SM00141; PDGF; 1.
DR  PROSITE; PS00249; PDGF_1; 1.
DR  PROSITE; PS02078; PDGF_2; 1.
KW  Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW  Heparin-binding; Multigene family.
FT  SIGNAL 1 26
FT  CHAIN 27 190 VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT  DISULFID 51 93
FT  DISULFID 82 127
FT  DISULFID 86 129
FT  DISULFID 76 76
FT  DISULFID 85 85
FT  CARBOHYD 100 100 N-LINKED (GLCNAC...) (POTENTIAL).
SQ  SEQUENCE 190 AA; 22276 MW; F00C5A8EA79A465F CRC64;

Query Match 84.0%; Score 665.5; DB 1; Length 190;
Best Local Similarity 85.0%; Pred. No. 7.7e-63;
Matches 119; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

Qy 1 MNFLSWVHSLALLYLHAKWSQAAPMAEGGQNHVEVVKFMDVYQSYCHPIETLVD 60
Db 1 MNFLSWVHSLALLYLHAKWSQAAPMAEGGQNHVEVVKFMDVYQSYCHPIETLVD 59

Qy 61 IFQYPPDEIEYIFRPSVPLMRCGCCNDEGLECVPTESNITMQIMRKPQSOHIGEM 120
Db 60 IFQYPPDEIEYIFRPSVPLMRCGCCNDEGLECVPTESNITMQIMRKPQSOHIGEM 119

Qy 121 SFLOHNKCECRPKKDRARQE 140
Db 120 SFLOHRCRCRPPKVRKPE 139

RESULT 10
VEGA_CHICK STANDARD; PRT; 216 AA.
AC P52582; Q91420;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor A precursor (VEGF-A) (Vascular
DE permeability factor) (VFP).
GN VEGF OR VEGFA.
OS Gallus gallus (Chicken), and
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031, 93934;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Chicken; TISSUE=Heart;
RA Takahashi T.;
RT "Chick embryonic ventricular myocytes VEGF.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=C.c.japonica; TISSUE=Embryo;
RX MEDLINE=96005007; Pubmed=7556923;
RA Flame I., von Reuten M., Drexler H.C., Syed-Ali S., Risau W.;
RT "Overexpression of vascular endothelial growth factor in the avian
RT embryo induces hypervascularization and increased vascular
RT permeability without alterations of embryonic pattern formation.";
RL Dev. Biol. 171:399-414(1995).
RN [3]
RP SEQUENCE OF 60-187 FROM N.A.
RC SPECIES=C.c.japonica;

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RX MEDLINE=95301109; Pubmed=7781909;
RA Flame I., Breier G., Risau W.;
RT "Vascular endothelial growth factor (VEGF) and VEGF receptor 2
RT (Flk-1) are expressed during vasculogenesis and vascular
RT differentiation in the quail embryo.";
RL Dev. Biol. 169:699-712(1995).
CC -!- FUNCTION: Growth factor active in angiogenesis, vasculogenesis and
CC endothelial cell growth. It induces endothelial cell
CC proliferation, promotes cell migration, inhibits apoptosis, and
CC induces permeabilization of blood vessels. It binds to the
CC VEGFR1/Flt-1 and VEGFR2/Kdr receptors and to heparan sulfate and
CC heparin (By similarity).
CC -!- SUBUNIT: Homodimer; disulfide-linked. Also found as heterodimer
CC with PlGF (By similarity).
CC -!- ALTERNATIVE PRODUCTS: At least 3 isoforms; VEGF190 (shown here),
CC VEGF166 and VEGF146; are produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: Abundantly and equally expressed in heart and
CC liver. In kidney glomeruli, brain and yolk sac, VEGF166 is 5- to
CC 10-times more abundant than VEGF190.
CC -!- DEVELOPMENTAL STAGE: VEGF166 is expressed early at day 1 and is
CC upregulated during gastrulation. Expression of VEGF190 is detectable
CC only from day 2.
CC -!- DOMAIN: VEGF190 contains a basic insert which acts as a cell
CC retention signal.
CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
DR EMBL; AB011078; BAA24925.1; -
DR EMBL; S79680; AAB35371.1; -
DR HSSP; P15692; 1VGH.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF_1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS02078; PDGF_2; 1.
KW Mitogen; Angiogenesis; Growth factor; Glycoprotein; Signal;
KW Heparin-binding; Alternative splicing; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 216 VASCULAR ENDOTHELIAL GROWTH FACTOR A.
FT DISULFID 52 94
FT DISULFID 83 128
FT DISULFID 87 130
FT DISULFID 77 77
FT DISULFID 86 86
FT CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPLIC 142 142 K -> N (IN ISOFORM VEGF-166).
FT VARSPLIC 143 166 MISSING (IN ISOFORM VEGF-166).
FT VARSPLIC 166 166 F -> L (IN ISOFORM VEGF-146).
FT VARSPLIC 167 210 MISSING (IN ISOFORM VEGF-146).
SQ SEQUENCE 216 AA; 25203 MW; 82E669C2F6FC6DA7 CRC64;

Query Match 70.1%; Score 555.5; DB 1; Length 216;
Best Local Similarity 68.3%; Pred. No. 3.2e-51;
Matches 97; Conservative 20; Mismatches 24; Indels 1; Gaps 1;

Qy 1 MNFLSWVHSLALLYLHAKWSQAAPMAEGGQNHVEVVKFMDVYQSYCHPIETLVD 60
Db 1 MNFLSWVHSLALLYLHAKWSQAAPMAEGGQNHVEVVKFMDVYQSYCHPIETLVD 60

Qy 61 IFQYPPDEIEYIFRPSVPLMRCGCCNDEGLECVPTESNITMQIMRKPQSOHIGEM 120
Db 61 IFQYPPDEIEYIFRPSVPLMRCGCCNDEGLECVPTESNITMQIMRKPQSOHIGEM 120

Qy 121 SFLOHNKCECRPKKDRARQE 141
Db 121 SFLOHRCRCRPPKVRKPE 141

```

[illegible]







RA Tucci M., Persico M.G., Acharya K.R.;  
 RT "the crystal structure of human placenta growth factor-1 (PLGF-1), an  
 RL angiogenic protein, at 2.0 Å resolution.";  
 RC J. Biol. Chem. 276:12153-12161(2001).  
 CC -!- FUNCTION: Growth factor active in angiogenesis, and endothelial  
 CC cell growth, stimulating their proliferation and migration. It  
 CC binds to receptor VEGFR-1/Flt1. PLGF-2 binds neuropilin-1 and 2 in  
 CC a heparin-dependent manner.  
 CC -!- SUBUNIT: Antiparallel homodimer; disulfide-linked. Also found as  
 CC heterodimer with VEGF/VEGF-A. PLGF-3 is found both as homodimer  
 CC and as monomer.  
 CC -!- SUBCELLULAR LOCATION: The three forms are secreted but PLGF-2  
 CC appears to remain cell attached unless released by heparin.  
 CC -!- ALTERNATIVE PRODUCTS: 3 isoforms; PLGF-1/PLGF-131, PLGF-2/PLGF-152  
 CC and PLGF-3 (shown here); are produced by alternative splicing.  
 CC -!- TISSUE SPECIFICITY: While the three forms are present in most  
 CC placental tissues, the PLGF-2 is specific to early (8 week)  
 CC placenta and only PLGF-1 is found in the colon and mammary  
 CC carcinomas.  
 CC -!- DOMAIN: PLGF-2 contains a basic insert which acts as a cell  
 CC retention signal.  
 CC -!- PTM: N-GLYCOSYLATED.  
 CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; X54936; CAA38698.1; -;  
 CC EMBL; S72960; AAB30462.2; -;  
 CC EMBL; S57152; AAB25832.2; ALT\_SEQ.  
 CC EMBL; AC006530; AAD30179.1; -;  
 CC EMBL; BC001422; AAH01422.1; -;  
 CC EMBL; BC007789; AAH07789.1; -;  
 CC EMBL; BC007255; AAH07255.1; -;  
 CC EMBL; AL8411; CAA01393.1; -;  
 CC DB: JF2V; 09-MAY-01.  
 CC Genew; HGNC:8893; PGF.  
 CC MIM; 601121; -;  
 CC InterPro; IPR000072; PD\_growth\_factor.  
 CC Pfam; PF00341; PDGF; 1.  
 CC ProDom; PD001629; PD\_growth\_factor; 1.  
 CC SMART; SM00141; PDGF; 1.  
 CC PROSITE; PS00249; PDGF\_1; 1.  
 CC PROSITE; PS0278; PDGF\_2; 1.  
 CC Mitogen; Growth factor; Glycoprotein; Signal; Heparin-binding;  
 CC Alternative splicing; 3D-structure.  
 CC SIGNAL 1 18  
 CC CHAIN 19 221 PLACENTA GROWTH FACTOR.  
 CC DOMAIN 193 213 HEPARIN-BINDING (PROBABLE).  
 CC DISULFID 52 94  
 CC DISULFID 83 128  
 CC DISULFID 87 130  
 CC DISULFID 77 77 INTERCHAIN.  
 CC DISULFID 86 86 INTERCHAIN.  
 CC DISULFID 33 33 N-LINKED (GLCNAC...) (POTENTIAL).  
 CC CARBOHYD 101 101 N-LINKED (GLCNAC...) (POTENTIAL).  
 CC VARSPLIC 132 203 MISSING (IN ISOFORM PLGF-1 AND ISOFORM  
 CC PLGF-2).  
 CC VARSPLIC 213 213 R -> RRRPKGRKRRRQRPTDCHL (IN ISOFORM  
 CC PLGF-2).  
 CC CONFLICT 91 91 N -> D (IN REF. 2).  
 CC SEQUENCE 221 AA; 24788 MW; D364C6A73C1C6987 CRC64;  
 CC  
 CC Query Match 38.9%; Score 308; DB 1; Length 221;  
 CC Best Local Similarity 47.0%; Pred. No. 3.2e-25;  
 CC Matches 54; Conservative 21; Mismatches 36; Indels 4; Gaps 1;  
 CC  
 CC 22 KWSQAAPMAEGGQNHHEVVKFMDVYQRSYCHPIETLVDFQYDEIEYIFKPSCVPLM 81

Db 26 OWALSA-----GNGSEVEVPFQEWGRSYCRALERLVDVYSEYSEVHMFSPSCVSL 81  
 Qy 82 RCGCCNDGEGECYPTESNTMTQIMRIKPHOGHIGEMSFLOHKNKCRPKKDR 136  
 Db 82 RCTGCCGDNLHCVPVETANVTMQLLKIRSGDRPSYVELTFSQHVRCRCRHSR 136  
 RESULT 15  
 PGLE\_RAT PGLE\_RAT STANDARD; PRT; 158 AA.  
 ID Q63434;  
 AC 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Placenta growth factor precursor (PIGF).  
 GN PIGF.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=95221439; PubMed=7706320;  
 RA Disalvo J., Bayne M.L., Conn G., Kwok P.W., Trivedi P.G.,  
 RA Soderman D.D., Palisi T.M., Sullivan K.A., Thomas K.A.;  
 RT "Purification and characterization of a naturally occurring vascular  
 RT endothelial growth factor/placenta growth factor heterodimer.";  
 RL J. Biol. Chem. 270:7717-7723(1995).  
 CC -!- FUNCTION: Growth factor active in angiogenesis, and endothelial  
 CC cell growth, stimulating their proliferation and migration. It  
 CC binds to receptor VEGFR-1/Flt1 (by similarity).  
 CC -!- SUBUNIT: Antiparallel homodimer; disulfide-linked. Also found as  
 CC heterodimer with VEGF/VEGF-A.  
 CC -!- SUBCELLULAR LOCATION: Secreted (by similarity).  
 CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
 CC  
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 CC  
 CC EMBL; L40030; AAA97426.1; -;  
 CC HSPF; P49763; IF2V.  
 CC InterPro; IPR000072; PD\_growth\_factor.  
 CC Pfam; PF00341; PDGF; 1.  
 CC ProDom; PD001629; PD\_growth\_factor; 1.  
 CC SMART; SM00141; PDGF; 1.  
 CC PROSITE; PS00249; PDGF\_1; 1.  
 CC PROSITE; PS0278; PDGF\_2; 1.  
 CC Mitogen; Growth factor; Glycoprotein; Signal.  
 CC SIGNAL 1 23  
 CC CHAIN 24 158 PLACENTA GROWTH FACTOR.  
 CC DISULFID 48 90 INTRACHAIN (BY SIMILARITY).  
 CC DISULFID 79 125 INTRACHAIN (BY SIMILARITY).  
 CC DISULFID -83 127 INTRACHAIN (BY SIMILARITY).  
 CC DISULFID 73 73 INTERCHAIN (BY SIMILARITY).  
 CC DISULFID 82 82 INTERCHAIN (BY SIMILARITY).  
 CC CARBOHYD 29 29 N-LINKED (GLCNAC...) (POTENTIAL).  
 CC CARBOHYD 30 30 N-LINKED (GLCNAC...).  
 CC CARBOHYD 97 97 N-LINKED (GLCNAC...).  
 CC SEQUENCE 158 AA; 17681 MW; B4771373A82E15B9 CRC64;  
 CC  
 CC Query Match 37.1%; Score 294; DB 1; Length 158;  
 CC Best Local Similarity 48.7%; Pred. No. 6.5e-24;  
 CC Matches 58; Conservative 19; Mismatches 40; Indels 2; Gaps 2;  
 CC  
 CC 24 SQAAPMAEGGQNHHEVVKFMDVYQRSYCHPIETLVDFQYDEIEYIFKPSCVPLMRC 83  
 Db 21 SQGA-LSAGNNSTEMEVYVFNVEVGRSYCRPMKLVYIADEHPNEVSHFSPSCVLLSRC 79

Oy 84 GGCNDEGLECVPTESNITMIMRIKPHQGH-IGEMSFLOHNKCECRPKKDRARQEK 141  
Db 80 SGGCGDEGLHCVALKTANITWILKIPNRPDHSYVENTFSQDVLCRCRPILETTKAER 138

Search completed: November 20, 2002, 04:57:29  
Job time : 39 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 20, 2002, 04:17:14 ; Search time 85 Seconds  
(without alignments)  
341.796 Million cell updates/sec

Title: US-09-884-050-2

Perfect score: 792

Sequence: 1 MNFLSWHWSLALLYLHH.....FLQHNKCEPRKKDRARQEK 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	787	99.4	191	4 Q96L82	Q96L82 homo sapien
2	787	99.4	191	4 Q96K10	Q96K10 homo sapien
3	787	99.4	191	6 Q95NE5	Q95NE5 macaca fasc
4	714.5	90.2	190	6 Q77643	Q77643 ovis aries
5	708.5	89.5	189	6 Q95LQ4	Q95LQ4 felis silve
6	703	88.8	126	6 Q9BDP7	Q9BDP7 macaca mula
7	695.5	87.8	190	11 Q9QX39	Q9QX39 spalax leuc
8	680.5	85.9	190	11 Q91ZE1	Q91ZE1 rattus norv
9	575.5	72.7	124	6 Q8SPZ9	Q8SPZ9 sus scrofa
10	561.5	70.9	118	6 Q9MZB1	Q9MZB1 ovis aries
11	555	70.1	124	6 Q9GK00	Q9GK00 callithrix
12	536.5	67.7	148	13 Q42571	Q42571 xenopus lae
13	536	67.7	128	6 Q8SPL5	Q8SPL5 equus cabal
14	532	67.2	127	6 Q8WMQ4	Q8WMQ4 sus scrofa
15	531.5	67.1	194	13 Q42572	Q42572 xenopus lae
16	510.5	64.5	141	11 Q70123	Q70123 mus musculu

```

17 482 60.9 142 11 Q9ERL6 Q9erl6 mesocricetu
18 422 53.3 78 6 Q9N1S2 Q9n1s2 capreolus c
19 422 53.3 123 6 Q9N1S1 Q9n1s1 capreolus c
20 409 51.6 75 6 O18843 O18843 oryctolagus
21 391 49.4 144 13 Q73822 Q73822 brachydanio
22 389 49.1 188 13 Q73682 Q73682 brachydanio
23 376 47.5 110 11 O88911 O88911 rattus norv
24 339 42.8 68 6 O97500 O97500 oryctolagus
25 297.5 37.6 146 13 Q90X23 Q90x23 bothrops ja
26 286.5 36.2 146 13 Q90X24 Q90x24 bothrops in
27 264 33.3 188 4 Q8TEV2 Q8tev2 homo sapien
28 252 31.8 132 12 Q9YMF3 Q9ymf3 orf virus.
29 185 23.4 418 13 Q57352 Q57352 coturnix co
30 184.5 23.3 326 11 Q91ZE6 Q91ze6 meriones un
31 184.5 23.3 415 11 Q91ZE3 Q91ze3 rattus norv
32 183 23.1 420 6 Q9XS50 Q9xs50 bos taurus
33 166.5 21.0 326 11 Q91ZE4 Q91ze4 rattus norv
34 157 19.8 102 6 Q9XT61 Q9xt61 macaca fasc
35 147.5 18.6 252 13 Q8QGD7 Q8qgd7 gallus gall
36 135.5 17.1 301 5 Q9VWP6 Q9vwp6 drosophila
37 135.5 17.1 314 5 Q9BLX1 Q9blx1 drosophila
38 135.5 17.1 325 5 Q960Z8 Q960z8 drosophila
39 135 17.0 89 11 Q91V66 Q91v66 rattus norv
40 131 16.5 23 11 Q91V21 Q91v21 rattus norv
41 130 16.4 65 11 Q91V68 Q91v68 rattus norv
42 130 16.4 102 11 Q63672 Q63672 rattus norv
43 123 15.5 22 4 Q9UN58 Q9uns8 homo sapien
44 120 15.2 23 11 Q91ZE2 Q91ze2 rattus norv
45 120 15.2 126 6 Q8WNS5 Q8wns5 bos taurus

```

#### ALIGNMENTS

RESULT 1

Q96L82 PRELIMINARY; PRT; 191 AA.

```

AC Q96L82;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Vascular endothelial growth factor.
GN VEGF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RT "Cloning of vascular endothelial growth factor (VEGF) cDNA.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY047581; AAK95847.1; -
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR PROSITE; PS00249; PDGF_1; UNKNOWN_1.
DR PROSITE; PS02078; PDGF_2; 1.
SQ SEQUENCE 191 AA; 22314 MW; CCE57097DD3779BD CRC64;

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Query Match 99.4%; Score 787; DB 4; Length 191;  
Best Local Similarity 100.0%; Pred. No. 2.9e-80;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
   |||||
Db 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
   |||||
QY 61 IQEYVDETEYIFKPSCVPLMRCGGCCNDGECVPTESNITMIMRKPHQGHIGEM 120
   |||||
Db 61 IQEYVDETEYIFKPSCVPLMRCGGCCNDGECVPTESNITMIMRKPHQGHIGEM 120
   |||||
QY 121 SPLQHNKCEPRKKDRARQE 140

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Db 121 SFLQHNKCECRPKKDRARQE 140
|||||
RESULT 2
Q96KJ0
ID Q96KJ0 PRELIMINARY; PRT; 191 AA.
AC Q96KJ0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor 165b.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Sugiono M., Winkler M., Gillatt D., Harper S.J., Bates D.O.;
RT "A new isoform of vascular endothelial growth factor mRNA is down-
regulated in renal tumors.";
RL (In) Unknown A. (eds.);
RL Proceedings of the 7th World Congress on Microcirculation, pp.3-3,
RL Sydney, Australia (2001).
RL EMBL; AF430806; AAL27435.1; -.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR PROSITE; PS00249; PDGF_1; UNKNOWN_1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 191 AA; 22258 MW; D25243E540AC79BD CRC64;

Query Match 99.4%; Score 787; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 2.9e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
|||||
Db 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
|||||
QY 61 IFQEYPDEIEYIFKPCVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHOGHIGEM 120
|||||
Db 61 IFQEYPDEIEYIFKPCVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHOGHIGEM 120
|||||
QY 121 SFLQHNKCECRPKKDRARQE 140
|||||
Db 121 SFLQHNKCECRPKKDRARQE 140
|||||

RESULT 3
Q95NE5
ID Q95NE5 PRELIMINARY; PRT; 191 AA.
AC Q95NE5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE SimVEGF165.
GN SIMVEGF165.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96245208; PubMed=8641836;
RA Shima D.T., Gougos A., Miller J.W., Tolentino M., Robinson G.,
RA Adams A.P., D'Amore P.A.;
RT "Cloning and mRNA expression of vascular endothelial growth factor in
ischemic retinas of Macaca fascicularis.";
RL Invest. Ophthalmol. Vis. Sci. 37:1334-1340(1996).
DR EMBL; S82167; AAB47118.1; -.

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DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR PROSITE; PS00249; PDGF_1; UNKNOWN_1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 191 AA; 22314 MW; CCE57097DD3779BD CRC64;

Query Match 99.4%; Score 787; DB 6; Length 191;
Best Local Similarity 100.0%; Pred. No. 2.9e-80;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
|||||
Db 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
|||||
QY 61 IFQEYPDEIEYIFKPCVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHOGHIGEM 120
|||||
Db 61 IFQEYPDEIEYIFKPCVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHOGHIGEM 120
|||||
QY 121 SFLQHNKCECRPKKDRARQE 140
|||||
Db 121 SFLQHNKCECRPKKDRARQE 140
|||||

RESULT 4
Q77643
ID Q77643 PRELIMINARY; PRT; 190 AA.
AC Q77643;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor.
GN VEGF.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA-RAMBOULLIET;
RA Cheung C.Y., Brace R.A.;
RT "Ovine vascular endothelial growth factor: Nucleotide sequence and
expression in fetal tissues.";
RL Growth Factors 0:0-0(1998).
DR EMBL; AF071015; AAC23608.1; -.
DR HSP; P15692; 1VGH.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 190 AA; 22342 MW; 0D5E3B3E5C53E739 CRC64;

Query Match 90.2%; Score 714.5; DB 6; Length 190;
Best Local Similarity 92.1%; Pred. No. 3.9e-72;
Matches 129; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
|||||
Db 1 MNFLSWHWSLALLYLHHAKWSQAAPMAE-GGQKPEVVKFMDVYQSYCHPIETLVD 59
|||||
QY 61 IFQEYPDEIEYIFKPCVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHOGHIGEM 120
|||||
Db 60 IFQEYPDEIEYIFKPCVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHOGHIGEM 119
|||||
QY 121 SFLQHNKCECRPKKDRARQE 140
|||||
Db 120 SFLQHNKCECRPKKDRARQE 139
|||||

RESULT 5

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Q95LQ4
ID Q95LQ4; PRELIMINARY; PRT; 189 AA.
AC Q95LQ4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Koga L., Kobayashi Y., Yazawa M., Masuda K., Ohno K., Tsujimoto H.;
RT "Nucleotide sequence and expression of the feline vascular endothelial
RT growth factor."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB071947; BAB68520.1; -.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR PROSITE; PS00249; PDGF_1; UNKNOWN_1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 189 AA; 22193 MW; C1E4646759AB3FD6 CRC64;

Query Match 89.5%; Score 708.5; DB 6; Length 189;
Best Local Similarity 92.1%; Pred. No. 1.8e-71;
Matches 128; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
Db 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 59
QY 61 IFQYEPDEIYIFKPCVPLMRGCGCNDGECVPTESNITQIMRIKPHOGQHIGEM 120
Db 60 IFQYEPDEIYIFKPCVPLMRGCGCNDGECVPTESNITQIMRIKPHOGQHIGEM 119
QY 121 SFLQHNKCECRPKKDRARQ 139
Db 120 SFLQHSKCECRPKKDRAKE 138

RESULT 6
Q9BDP7
ID Q9BDP7; PRELIMINARY; PRT; 126 AA.
AC Q9BDP7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Hazzard T.M., Navak N.R., Jia Y., Stouffer R.L.;
RT "Rhesus macaque VEGF mRNA sequence."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF337373; AAK26379.1; -.
DR HSSP; PI5692; 2VPF.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
FT NON_TER 1
FT NON_TER 126
SQ SEQUENCE 126 AA; 14599 MW; 1175F2386A883BCF CRC64;

Query Match 88.8%; Score 703; DB 6; Length 126;

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Best Local Similarity 99.2%; Pred. No. 4.8e-71;
Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 VHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVDIFQEYPD 67
Db 1 VHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVDIFQEYPD 60
QY 68 EIEYIFKPCVPLMRGCGCNDGECVPTESNITQIMRIKPHOGQHIGEMSFLQHNK 127
Db 61 EIEYIFKPCVPLMRGCGCNDGECVPTESNITQIMRIKPHOGQHIGEMSFLQHNK 120
QY 128 CECRPK 133
Db 121 CECRPK 126

RESULT 7
Q9QX39
ID Q9QX39; PRELIMINARY; PRT; 190 AA.
AC Q9QX39;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor.
GN VEGF.
OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;
OC Nannospalax.
OX NCBI_TaxID=30637;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99313148; PubMed=10386577;
RA Avivi A., Resnick M.B., Nevo E., Joel A., Levy A.P.;
RT "Adaptive hypoxic tolerance in the subterranean mole rat Spalax
RT ehrenbergi: the role of vascular endothelial growth factor."
RL FEBS Lett. 452:133-140(1999).
DR EMBL; AF186236; AAD56245.1; -.
DR HSSP; PI5692; 2VPF.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 190 AA; 22488 MW; 2228383BC65F0BFE CRC64;

Query Match 87.8%; Score 695.5; DB 11; Length 190;
Best Local Similarity 89.3%; Pred. No. 5.2e-70;
Matches 125; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
Db 1 MNFLSWHWSLALLYLHHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 59
QY 61 IFQYEPDEIYIFKPCVPLMRGCGCNDGECVPTESNITQIMRIKPHOGQHIGEM 120
Db 60 IFQYEPDEIYIFKPCVPLMRGCGCNDGECVPTESNITQIMRIKPHOGQHIGEM 119
QY 121 SFLQHNKCECRPKKDRARQ 140
Db 120 SFLQHNKCECRPKKDRTRLE 139

RESULT 8
Q91ZEI
ID Q91ZEI; PRELIMINARY; PRT; 190 AA.
AC Q91ZEI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor.
GN VEGF.

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Marion S., Lee T.-C.;
RT "Cloning of multiple VEGF splice variants from hypoxic neonatal rat
cardiomyocytes.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY033506; AAL07526.1; -.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR PROSITE; PS00249; PDGF_1; UNKNOWN_1.
DR PROSITE; PS50278; PDGF_2; 1.
SQ SEQUENCE 190 AA; 2396 MW; 589374010441F377 CRC64;

Query Match 85.9%; Score 680.5; DB 11; Length 190;
Best Local Similarity 87.1%; Pred. No. 2.5e-68;
Matches 122; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 MNFLLSWVHSLALLLHLHAKWSQAAPMAEGGQNHHEVVKFMDVYQSYCHPIETLVD 60
D 1 MNFLLSWVHSLALLLHLHAKWSQAAPTE-GEQKAHEVVKFMDVYQSYCHPIETLVD 59
QY 61 IFQYEPDEIEYIFKPSVPLMRCGCCNDEGLECVPTESNITMQIMRIKPHQSHIGEM 120
D 60 IFQYEPDEIEYIFKPSVPLMRCAGCCNDEALECVPTESNITMQIMRIKPHQSHIGEM 119
QY 121 SFLOHNCCEPRKKDRARQE 140
D 120 SFLOHRCCEPRKKDKTKE 139

RESULT 9
Q8SP29 PRELIMINARY; PRT; 124 AA.
AC Q8SP29;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MYOCARDIUM;
RA Yuan H., Li J.;
RT "The expression of VEGF in porcine collateral-dependent myocardial by
exercise training.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461807; AAL85286.1; -.
DR NON_TER 124 124
SQ SEQUENCE 124 AA; 14552 MW; 2E1C1A009E67C9C9 CRC64;

Query Match 72.7%; Score 575.5; DB 6; Length 124;
Best Local Similarity 94.6%; Pred. No. 9.1e-57;
Matches 106; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 29 MAEGGQNHHEVVKFMDVYQSYCHPIETLVDIFQYEPDEIEYIFKPSVPLMRCGCCN 88
D 1 MAE-GDQKPEHVVKFMDVYQSYCHPIETLVDIFQYEPDEIEYIFKPSVPLMRCGCCN 59

QY 89 DEGLECVPTESNITMQIMRIKPHQSHIGEMSFLOHNCCEPRKKDRARQE 140
D 60 DEGLECVPTESNITMQIMRIKPHQSHIGEMSFLOHNCCEPRKKDRARQE 111

RESULT 10
Q8SP29 PRELIMINARY; PRT; 124 AA.
AC Q8SP29;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MYOCARDIUM;
RA Yuan H., Li J.;
RT "The expression of VEGF in porcine collateral-dependent myocardial by
exercise training.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461807; AAL85286.1; -.
DR NON_TER 124 124
SQ SEQUENCE 124 AA; 14552 MW; 2E1C1A009E67C9C9 CRC64;

Query Match 72.7%; Score 575.5; DB 6; Length 124;
Best Local Similarity 94.6%; Pred. No. 9.1e-57;
Matches 106; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 29 MAEGGQNHHEVVKFMDVYQSYCHPIETLVDIFQYEPDEIEYIFKPSVPLMRCGCCN 88
D 1 MAE-GDQKPEHVVKFMDVYQSYCHPIETLVDIFQYEPDEIEYIFKPSVPLMRCGCCN 59

QY 89 DEGLECVPTESNITMQIMRIKPHQSHIGEMSFLOHNCCEPRKKDRARQE 140
D 60 DEGLECVPTESNITMQIMRIKPHQSHIGEMSFLOHNCCEPRKKDRARQE 111

RESULT 11
Q9GK00 PRELIMINARY; PRT; 124 AA.
AC Q9GK00;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
GN VEGF.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVIDUCT;
RA Welter H., Gabler C., Einspanier R.;
RT "growth factor expression in marmoset monkey oviducts.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ278192; CAC19923.1; -.
DR HSSP; P15692; IVGH.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR NON_TER 1 1
FT NON_TER 124 124

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Q9MZB1 PRELIMINARY; PRT; 118 AA.
AC Q9MZB1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
GN VEGF.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTAL ARTERY ENDOTHELIUM;
RA Zheng J., Tsou S.C., Magness R.R.;
RT "Growth factor expression in ovine fetal placental artery endothelial
cells.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF250375; AAF75258.1; -.
DR HSSP; P15692; IVPP.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR NON_TER 1 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 13931 MW; 757DC59AA56378A6 CRC64;

Query Match 70.9%; Score 561.5; DB 6; Length 118;
Best Local Similarity 90.3%; Pred. No. 3.2e-55;
Matches 102; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 29 MAEGGQNHHEVVKFMDVYQSYCHPIETLVDIFQYEPDEIEYIFKPSVPLMRCGCCN 88
D 1 MAE-GGQKPEHVVKFMDVYQSYCHPIETLVDIFQYEPDEIEYIFKPSVPLMRCGCCN 59

QY 89 DEGLECVPTESNITMQIMRIKPHQSHIGEMSFLOHNCCEPRKKDRARQE 141
D 60 DEGLECVPTESNITMQIMRIKPHQSHIGEMSFLOHNCCEPRKKDRARQE 112

RESULT 11
Q9GK00 PRELIMINARY; PRT; 124 AA.
AC Q9GK00;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
GN VEGF.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVIDUCT;
RA Welter H., Gabler C., Einspanier R.;
RT "growth factor expression in marmoset monkey oviducts.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ278192; CAC19923.1; -.
DR HSSP; P15692; IVGH.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
DR NON_TER 1 1
FT NON_TER 124 124

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OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-ENDOMETRIUM;
RA Welter H., Bollwein H., Einspanier R.;
RT "Expression of horse endometrium.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RD EMBL; AJ439887; CAD29178.1; -.
RE FT NON_TER 1
FT NON_TER 128
SQ SEQUENCE 128 AA; 14943 MW; 64EFA5DB550FC638 CRC64;

Query Match 67.7%; Score 536; DB 6; Length 128;
Best Local Similarity 94.1%; Pred. No. 2.5e-52;
Matches 96; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 39 EVVKFMDVYORSCHPIETLVDFIQEYDDEIYIFKPSVPLMRGCGCCNDGEGLCVPT 98
DB 1 EVVKFMDVYORSCHPIETLVDFIQEYDDEIYIFKPSVPLMRGCGCCNDGEGLCVPTA 60
QY 99 ESNITQIMRIKPHQGHIGEMSFLOHNKCECRPKKDRARQE 140
DB 61 EFNITQIMRIKPHQGHIGEMSFLOHNKCECRPKKDRARQE 102

RESULT 14
Q8WNQ4
ID Q8WNQ4 PRELIMINARY; PRT; 127 AA.
AC Q8WNQ4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MYOCARDIUM;
RA Yuan H., Li J.;
RT "The expression of VEGF in porcine collateral-dependent myocardial by
exercise training.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RD EMBL; AY072734; AAL68393.1; -.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; UNKNOWN_1.
DR PROSITE; PS50278; PDGF_2; 1.
FT NON_TER 127
SQ SEQUENCE 127 AA; 14920 MW; 5AB63F01AEB29ED CRC64;

Query Match 67.2%; Score 532; DB 6; Length 127;
Best Local Similarity 96.9%; Pred. No. 7e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 44 MDVYQSYCHPIETLVDFIQEYDDEIYIFKPSVPLMRGCGCCNDGEGLCVPTESNIT 103
DB 1 MDVYQSYCHPIETLVDFIQEYDDEIYIFKPSVPLMRGCGCCNDGEGLCVPTEFNIA 60
QY 104 MQIMRIKPHQGHIGEMSFLOHNKCECRPKKDRARQE 141
DB 61 MQIMRIKPHQGHIGEMSFLOHNKCECRPKKDRARQE 98

RESULT 15
O42572
ID O42572 PRELIMINARY; PRT; 194 AA.
AC O42572;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

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DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Vascular endothelial growth factor 196.
GN VEGF.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Cleaver O., Tonissen K.F., Saha M.S., Krieg P.A.;
RT "Neovascularization of the Xenopus embryo.";
RL Dev. Dyn. 0:0-0(1997).
DR EMBL; AF008594; AAB63680.1; -.
DR HSSP; P15692; LVGH.
DR InterPro; IPR000072; PD_growth_factor.
DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PD_growth_factor; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
DR PROSITE; PS0278; PDGF_2; 1.
SQ SEQUENCE 194 AA; 22672 MW; 85D7BEC7CEFEF17E CRC64;

Query Match 67.1%; Score 531.5; DB 13; Length 194;
Best Local Similarity 69.5%; Pred. No. 1.3e-51;
Matches 98; Conservative 15; Mismatches 27; Indels 1; Gaps 1;

QY 1 MNFLLSVHWWSLALLYLHAKWSQAPMAEGGQNNHVVKPMVYQRSYCHPIETLVD 60
Db 1 MNFLPSWIHWGLAVLLYIPHAQLSGAAPMGEGDHRKPTVVKFKVYERSMCQVRELLVD 60

QY 61 IFQEYDEIEYIFKPSVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHQGHIGEM 120
Db 61 IFQEYDEVEYIFKPSVPLMRGCGCCNDEGLECVPTESNITMQIMRIKPHISQHIMDM 120

QY 121 SFLQHNKCECRPKKD-RAROE 140
Db 121 SFOQHSQCECRPKRKEVKSKE 141
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Search completed: November 20, 2002, 04:59:26  
Job time : 95 secs



GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 20, 2002, 04:58:43 ; Search time 273 Seconds  
(without alignments)  
1163.120 Million cell updates/sec

Title: US-09-884-050-2  
Perfect score: 792  
Sequence: 1 MNFLSWVHWSALLLLYHH.....FLQHNKCECRPKKDRARQEK 141

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+B2n.model -DEV=xlh  
-O/Cyn2\_1/USPFO\_pool/US09884050/runat\_13112002\_133001\_14104/app\_query.fasta\_1.327  
-DB=N.Geneseq\_101002 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09884050 -ACGN\_1\_1\_0 -runat\_13112002\_133001\_14104 -NCPU=6 -ICPU=3  
-NO\_XLPXY -NO\_MAP -LARGQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N.Geneseq\_101002.\*

1: /SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
3: /SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.\*  
4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.\*  
5: /SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.\*  
6: /SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.\*  
7: /SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.\*  
8: /SID22/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.\*  
9: /SID22/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.\*  
10: /SID22/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.\*  
11: /SID22/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.\*  
12: /SID22/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.\*  
13: /SID22/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.\*  
14: /SID22/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.\*  
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17: /SID22/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.\*  
18: /SID22/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.\*  
19: /SID22/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.\*  
20: /SID22/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.\*  
21: /SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.\*  
22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*  
23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	792	100.0	441	19	AAV38450	cDNA encoding huma
2	792	100.0	444	21	AAZ93345	Human vascular end
3	792	100.0	444	21	AAZ93345	Nucleotide sequenc
4	792	100.0	444	22	AAZ93345	Human vascular end
5	792	100.0	444	22	AAZ93345	Human VEGF121 DNA.
6	792	100.0	444	24	ABL57427	Human vascular end
7	792	100.0	473	16	AAQ99080	cDNA encoding huma
8	792	100.0	473	17	AAZ17613	VEGF121 coding seq
9	792	100.0	473	21	AAZ12853	cDNA encoding VEGF
10	792	100.0	495	20	AAZ29996	Nucleotide sequenc
11	792	100.0	516	19	AAZ28396	Vascular endotheli
12	792	100.0	516	20	AAZ57724	Human VEGF(145) co
13	792	100.0	544	22	AAZ21876	Human VEGF splice
14	792	100.0	545	20	AAZ29999	Nucleotide sequenc
15	792	100.0	573	19	AAV38451	cDNA encoding huma
16	792	100.0	627	20	AAZ29997	Nucleotide sequenc
17	792	100.0	642	21	AAZ93348	Human vascular end
18	792	100.0	642	21	AAZ299547	Nucleotide sequenc
19	792	100.0	642	22	AAZ90480	Human VEGF189 DNA.
20	792	100.0	642	24	ABL57430	Human vascular end
21	792	100.0	645	19	AAV38452	cDNA encoding huma
22	792	100.0	648	21	AAZ39835	Human A215 nucleot
23	792	100.0	648	22	AAZ83521	Human VEGF C subun
24	792	100.0	666	20	AAZ29998	Nucleotide sequenc
25	792	100.0	677	16	AAQ99082	cDNA encoding huma
26	792	100.0	677	17	AAZ17615	VEGF189 coding seq
27	792	100.0	677	21	AAZ12855	cDNA encoding VEGF
28	792	100.0	696	21	AAZ38453	cDNA encoding huma
29	792	100.0	699	21	AAZ93349	Human vascular end
30	792	100.0	699	21	AAZ99548	Nucleotide sequenc
31	792	100.0	699	22	AAZ90481	Human VEGF206 DNA.
32	792	100.0	699	24	ABL57431	Human vascular end
33	792	100.0	728	16	AAQ99083	Human vascular end
34	792	100.0	728	17	AAZ17616	VEGF206 coding seq
35	792	100.0	728	21	AAZ12856	cDNA encoding VEGF
36	792	100.0	774	18	AAZ85644	Antisense inhibito
37	792	100.0	774	18	AAZ79139	Human vascular end
38	792	100.0	774	19	AAV15102	Human vascular end
39	792	100.0	774	19	AAZ95393	Human vascular end
40	792	100.0	815	22	AAZ12883	DNA encoding for h
41	792	100.0	1195	11	AAQ84474	Human vascular per
42	792	100.0	1195	20	AAZ90498	Human vascular end
43	792	100.0	1873	19	AAV15103	Human vascular end
44	792	100.0	1873	20	AAZ21568	Vascular endotheli
45	789	99.6	774	17	AAZ10120	Vascular endotheli

# ALIGNMENTS

## RESULT 1

AAV38450  
ID AAV38450 standard; cDNA; 441 BP.  
XX  
AC AAV38450;  
XX  
DT 11-SEP-1998 (first entry)  
XX  
DE cDNA encoding human VEGF-121.

XX Human; vascular endothelial growth factor; VEGF; production;  
XX nitric oxide; prostacyclin; treatment; prevention; intimal hyperplasia;  
XX blood vessel; essential hypertension; pulmonary arterial hypertension;  
XX PAH; cor pulmonale; atherosclerosis; (re)stenosis; angioplasty;  
XX coronary bypass operation; anastomosis; endarterectomy; ss.  
OS Homo sapiens.  
XX



KW	platelet aggregation; thrombosis; preeclampsia; sepsis; pancreatitis;
KW	intravascular coagulation; thrombotic thrombocytopenia purpura;
KW	acute renal failure; myocardial infarction; ischemic bowel disease;
KW	stroke; hypoxia; hypercapnia; fibrosis; toxic alveolar injury;
KW	acute respiratory distress syndrome; pneumonia; pulmonary emboli;
KW	birth prematurity disorder; wound; allergy; hypersensitivity;
KW	autoimmune disease; organ transplant; focal glomerulosclerosis;
XX	amyloidosis; ss.
XX	Homo sapiens.
XX	OS
XX	OS
FH	Key
FT	Location/Qualifiers
FT	1..444
FT	/*tag= a
FT	/product= "vascular endothelial growth factor 121"
XX	
XX	

[illegible]

XX  
27 MAY 1955, 0000 0120013.

PA (SCIO-) SCIOS INC.  
XX

PI  
Schreiner GF, Johnson RJ;  
XX

BR WPI; 2000-2568617  
DR P-PSDB: AAY69412

Novel methods and composition

PT microvascular angioopathies by administration of angiogenic factors  
as vascular endothelial growth factor (VEGF) -

XX  
PS Disclosure: Fig 2

xx The present sequence encodes nativ

Db 181 ATCTTCCAGGAGTACCTGTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCCCTG 340

81 MetArgCysGlvGlvCysCysAsnAspGlvGlvLeuGlvCysValProThrGlvGlvSer 100

D<sub>b</sub> 241 ATGCCGATGCGGGGGCTGCTGCAATGACCGAGGGGCTGGAGTGTGTGCCCACTGAGGAGTCC 300

101 AsnIleThrMetGlnIleMetArgTleLysProHisGlnGlyGlnHisTleGlyGlnMet 120

301 AACATCACCATGCAGATTATGCGGATCAAAACCTCACCAAGGCCACACATAGGAGAGATG 360

Ov 121 SerPheLeuGlnHisAsnLysCysGlnCysArgProLysIysAspArgAlaArgGlnGlu 140

361 AGCTTCCTACAGCACAACAAATGTGAAATGCAGACCAAGAAAGATAGAGCAAGACAAGAA 420

Ov 141 Lvs 141

Db 421 AAA 423

### RESULT 3

AAZ995344  
ID AAZ99544 standard: DNA: 444 BP.

AAZ99544:

03-JUL-2000 (first entry)

DE Nucleotide sequence of vascular endothelial growth factor 121

**KW** Human: vascular endothelial growth factor: VEGF 121: angiogenic factor

KW blood vessel injury; vascular injury; microvascular angiopathy;  
KW thrombotic microangiopathy; kidney disease: haemolytic uremic syndrome

kw  
toxic shock syndrome; venom; hypercoagulable state; platelet activation



KW vasotropic; antibacterial; angiogenesis; vascular remodelling;  
 KW vascular disease; kidney disease; diabetes; systemic lupus erythematosus;  
 KW meningitis; tumour; infection; lung disease inflammatory bowel disease;  
 KW ds.  
 XX Homo sapiens.  
 OS  
 PN WO200071713-A1.  
 XX  
 XX 30-NOV-2000.  
 XX  
 XX 18-MAY-2000; 2000WO-US13536.  
 PF  
 XX 20-MAY-1999; 99US-0135312.  
 PR  
 XX (SCIO-) SCIOS INC.  
 XX  
 XX Pollitt NS, Abraham JA;  
 PI  
 XX WPI; 2001-025162/03.  
 DR P-PSDB; AAB50431.  
 DR  
 XX  
 XX  
 PT Enhancing biological activity of vascular endothelial growth factor by  
 PT replacing a Cys residue, for producing variant useful for treating  
 PT hypertension, stroke, diabetes, lupus, glomerulonephritis, meningitis,  
 PT tumor, pneumonia, infections -  
 PT  
 XX  
 PS Disclosure; Fig 2; 62pp; English.  
 XX

CC The present sequence is given in a specification relating to a method for  
 CC enhancing the biological activity of a vascular endothelial growth factor  
 CC (VEGF) originally having a cysteine residue at a position 116 of the 121  
 CC amino acid native mature human VEGF. The method comprises eliminating the  
 CC cysteine residue to produce a VEGF variant. The variant is useful for  
 CC inducing angiogenesis or vascular remodelling, for prevention or repair  
 CC of injury to blood vessels, where injury is associated with haemolytic  
 CC uraemic syndrome (HUS) or microvascular angiopathy such as thrombotic  
 CC microangiopathy (TMA). The VEGF variant is also useful for treatment of  
 CC essential hypertension in a patient. The variant is useful for treating  
 CC coronary artery disease and/or peripheral arterial disease, to foster  
 CC myocardial blood vessel growth and to improve blood flow to the heart. It  
 CC is useful for the treatment and prevention of kidney diseases associated  
 CC with injury to, or atrophy of, the vasculature of the glomerulus and  
 CC interstitium and for the treatment and prevention of acute renal failure,  
 CC myocardial infarction, ischaemic bowel disease, transient ischaemic  
 CC attacks, stroke, hypoxia, hypercapnia, focal glomerulosclerosis,  
 CC amyloidosis, glomerulonephritis, diabetes, systemic lupus erythematosus  
 CC or chronic hypoxia/atrophy. It is also useful in the preservation or  
 CC enhancement of function of organ allografts and xenografts, and for  
 CC treating disorders related to abnormal transport of solutes across  
 CC endothelial cells such as meningitis, tumour, infections, disorders of  
 CC bone growth, acute respiratory distress syndrome, toxic alveolar injury,  
 CC pneumonia, cystic fibrosis, inflammatory bowel disease, infectious  
 CC diarrhoea or cardiac valve disease.  
 XX

SX Sequence 444 BP; 121 A; 113 C; 122 G; 88 T; 0 other;

Alignment Scores:  
 Pred. No.: 1,768-87 Length: 444  
 Score: 792.00 Matches: 141  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US-09-884-050-2 (1-141) x AAC90477 (1-444)

QY 1 MetAsnPhelLeuSerTrpValHisTrpSerLeuAlaLeuLeuLeuTrpHisHis 20  
 ||||||||||||||||||  
 Db 1 ATGAACCTTCTGCTGCTTGGTGATCGAGCCCTGCTGCTACCTCCACCAT 60  
 ||||||||||||||||||  
 QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40  
 ||||||||||||||||||

Db 61 GCCAAGTGGTCCAGGCTGCCACCCATGGCAGAAAGGAGGAGGCAGAAATCATCACGAAGTG 120  
 QY 41 VallysPheMetAspValTrpGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
 ||||||||||||||||||  
 Db 121 GTGAAGTTTCATGGATGCTATCAGCGCAGCTACTGCCATCCAAATCGAGACCTGGTGGAC 180  
 QY 61 IlePheGlnGluTrpProAspGluIleGluTrpIlePheLysProSerCysValProLeu 80  
 ||||||||||||||||||  
 Db 181 ATCTTCCAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCTCTGTGCCCCCTG 240  
 QY 81 MetArgCysGlyGlyCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
 ||||||||||||||||||  
 Db 241 ATCGATGCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCCACTGAGGAGTCC 300  
 QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
 ||||||||||||||||||  
 Db 301 AACATCACCATGCAGATTATGCGGATCAACCTCACCAGGCCAGCACATAGAGAGATG 360  
 QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
 ||||||||||||||||||  
 Db 361 AGCTTCTTACAGCACACAACAATGTGAATGCAGACCAAGAAAGATAGAGCAAGACAAGAA 420  
 QY 141 Lys 141  
 |||  
 Db 421 AAA 423  
 RESULT 6  
 ABL57427  
 ID ABL57427 standard; cDNA; 444 BP.  
 XX  
 AC ABL57427;  
 XX  
 DT 12-AUG-2002 (first entry)  
 XX  
 DE Human vascular endothelial growth factor 121 coding sequence.  
 XX  
 KW Vascular endothelial growth factor; VEGF; hVEGF121; human;  
 KW hypertension; hypotensive; nephrotropic; cerebroprotective;  
 KW antibacterial; cytostatic; antialcholic; virucide; vasotropic;  
 KW antiarrhythmic; immunosuppressive; cardiant; antiinflammatory;  
 KW angiogenic factor; gene; ss.  
 XX  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 CDS 1..444  
 FT /\*tag= a  
 FT /product= "hVEGF121"  
 FT 1..78  
 FT sig\_peptide /\*tag= b  
 FT mat\_peptide 79..441  
 FT /\*tag= c  
 XX  
 PN US6352975-B1.  
 XX  
 PD 05-MAR-2002.  
 XX  
 PF 09-SEP-1999; 99US-0392932.  
 XX  
 PR 09-SEP-1998; 98US-099694P.  
 PR 26-MAR-1999; 99US-126406P.  
 PR 27-MAR-1999; 99US-126615P.  
 XX  
 PA (SCIO-) SCIOS INC.  
 XX  
 PI Schreiner GF, Johnson RJ;  
 XX  
 DR WPI; 2002-412951/44.  
 DR P-PSDB; ABB76299.  
 XX  
 PT New method, useful in treatment of salt-sensitive hypertension,  
 PT comprises administration of a vascular endothelial growth factor to a  
 PT patient -

XX Disclosure; Fig 6; 30pp; English.

XX The present sequence is the coding sequence of human vascular

XX endothelial growth factor 121 (hVEGF121), an isoform that is weakly

XX acidic and does not bind to heparin. The present invention

XX concerns methods for the treatment of salt-sensitive hypertension

XX by administering a VEGF in an amount effective to reduce the blood

XX pressure of a salt-sensitive hypertension patient to a normal range.

XX The VEGF is preferably hVEGF121 or a VEGF having a heparin-binding

XX domain modified to render it incapable of binding heparin. The

XX VEGF may be co-administered with another angiogenic factor. The

XX method can also be used to treat disorders relating to abnormal

XX transport of solutes across endothelial cells, including treatment

XX or prevention of kidney disease associated with impaired filtration

XX or excretion of solutes, central nervous system diseases associated

XX with alterations in cerebrospinal fluid synthesis, composition or

XX circulation including stroke, meningitis, tumour, infections, and

XX disorders of bone growth, hypoxia or hypercapnia or fibrosis

XX arising from accumulation of fluid secretions in lungs or

XX impediments to their removal, including acute respiratory distress

XX syndrome, toxic alveolar injury as occurs in smoke inhalation,

XX pneumonia, including viral and bacterial infections, surgical

XX interventions, cystic fibrosis, and other inherited or acquired

XX disease of the lung associated with fluid accumulation in the

XX pulmonary air space, pulmonary endothelium injury, disordered

XX transport of fluid and solutes across the intestinal epithelium,

XX including inflammatory bowel disease, infections, diarrhoea,

XX ascites accumulation in the peritoneum as occurs in the failure of

XX heart, liver and kidney, preservation and enhancement of function

XX of organ allografts, and cardiac valve disease.

XX SQ Sequence 444 BP; 121 A; 113 C; 122 G; 88 T; 0 other;

Alignment Scores:

Pred. No.: 1.76e-87 Length: 444

Score: 792.00 Matches: 141

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 24 Gaps: 0

US-09-884-050-2 (1-141) x ABL57427 (1-444)

Qy 1 MetAsnPhLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuLeuHisHis 20

Db 1 ATGAATTTCTGCTGCTTGGTGATGGAGCCTTGCTGCTGCTACCTCCACCAT 60

Qy 21 AlalysTrpSerGlnAlaAlaPromMetAlaGluGlyGlyGlnAsnHisGluVal 40

Db 61 GCCAAGTGGTCCAGGCTGCACCCATGGCAGAGGAGGAGGAGATCATCAGGAATG 120

Qy 41 VallysPheMetAspValTrpGlnArgSerTrpCysHisProIleGluThrLeuValAsp 60

Db 121 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCTCCATCCATCAGACCCCTGGTGAC 180

Qy 61 IlePheGlnGluTrpProAspGluIleGluTrpIlePheLysProSerCysValProLeu 80

Db 181 ATCTTCCAGGAGTACCTGTGATGAGATGATGATGATGATGATGATGATGATGATG 240

Qy 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100

Db 241 ATGCGATCGGGGGTGTGTAATACGAGGGGCTGGAGTGTGTCCTCCAGGAGTCC 300

Qy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120

Db 301 AACATCACCATGCAATATGCGGATCAAACTCACCAGGCCACACATAGGAGATG 360

Qy 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140

Db 361 AGCTTCCTACAGCACACAATGTGAATGCAGACCAAGAAAGATAGACGAAGCAAGA 420

Qy 141 Lys 141

Db 421 AAA 423

RESULT 7

AAQ99080

ID AAQ99080 standard; cDNA; 473 BP.

XX

AC AAQ99080;

XX

DT 14-MAY-1996 (first entry)

XX

DE cDNA encoding human vascular endothelial growth factor-121, VEGF-121.

XX

KW Conjugate; growth factor; FGF; cytotoxin; saporin; eye; regulation;

XX

KW cell proliferation; psoriasis; pterygia; corneal clouding; cancer;

XX

KW rheumatoid arthritis; vascular endothelial; fibroblast; epidermal;

XX

OS Homo sapiens.

XX

FT Key Location/Qualifiers

XX

FT CDS 13..456

XX

FT /\*tag= a

XX

FT /product= immature\_VEGF-121

XX

FT sig\_peptide 13..90

XX

FT /\*tag= b

XX

FT mat\_peptide 91..453

XX

FT /\*tag= c

XX

PN WO9524928-A2.

XX

XX 21-SEP-1995.

XX

XX 15-MAR-1995; 95WO-US03448.

XX

XX 15-MAR-1994; 94US-0213447.

XX

XX 15-MAR-1994; 94US-0213446.

XX

PA (PRIZ-) PRIZM PHARM INC.

XX

PI Baird JA, Houston LL, Nova MP, Sosnowski BA;

XX

XX WPI: 1995-336820/43.

XX

DR P-PSDB: AAR91075.

XX

XX New conjugates of growth factor receptor ligand and targetted agent

XX

PT - partic. DNA or cytotoxin, used to control cell proliferation in

XX

PT the eye, e.g. to prevent growth of pterygia and corneal clouding

XX

PS Disclosure; Page 184-185; 204pp; English.

XX

XX AAQ99080-099083 encode human vascular endothelial growth factors

XX

CC (VEGFs). DNA encoding a VEGF can be used to create a fusion protein

XX

CC (FP), the cDNA of which includes a nucleic acid binding domain (NABD)

XX

CC and encodes a heparin binding growth factor, HGF (e.g. VEGF, FGF,

XX

CC HBGF), a protein synthesis inhibitor and opt. a linker imparting

XX

CC flexibility to the FP. The FP can be used to target a protein synthesis

XX

CC inhibitor, an antisense DNA sequence or an inhibitor of elongation factor

XX

CC 2, to a cell carrying a HGF receptor. The conjugates of the invention

XX

CC are used to inhibit cell proliferation in cells carrying the particular

XX

CC growth factor receptor. A specific application is to prevent

XX

CC excessive proliferation of epithelial cells, fibroblasts and

XX

CC keratinocytes in the anterior eye after surgery, partic. to prevent

XX

CC recurrence of pterygia after surgical removal, closure of

XX

CC trabeculectomy after glaucoma surgery and corneal clouding after

XX

CC excimer laser treatment. Other conditions which may be treated include

XX

CC tumours, restenosis, psoriasis, Dupuytren's contracture, diabetic

XX

CC complications, Kaposi's sarcoma and rheumatoid arthritis.

XX

SQ Sequence 473 BP; 131 A; 119 C; 130 G; 93 T; 0 other;

Alignment Scores: 1.93e-87 Length: 473

Pred. No.:



Db 433 AAA 435  
 RESULT 9  
 AAA12853  
 ID AAA12853 standard; cDNA; 473 BP.  
 XX  
 AC AAA12853;  
 XX  
 DT 18-JUL-2000 (first entry)  
 DE  
 DE cDNA encoding VEGF (clone VEGF121), SEQ ID NO:1.  
 XX  
 KW Targeted gene delivery; fibroblast growth factor receptor;  
 KW FGFR-binding protein; nucleic acid binding protein;  
 KW receptor-internalised ligand; cytotoxin; saporin; gene therapy;  
 KW cytocide; antiproliferative; cancer; melanoma; diabetic retinopathy;  
 KW rheumatoid arthritis; restenosis, Dupuytren's contracture; psoriasis;  
 KW eczema; heparin-binding epidermal growth factor; HBEGF;  
 KW vascular endothelial growth factor; VEGF; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN US6037329-A.  
 XX  
 XX 14-MAR-2000.  
 XX  
 XX 24-SEP-1996; 96US-0718904.  
 XX  
 XX 15-MAR-1994; 94US-0213446.  
 PR 15-MAR-1994; 94US-0213447.  
 PR 29-AUG-1994; 94US-0297961.  
 PR 13-SEP-1994; 94US-0305771.  
 PR 16-MAY-1995; 95US-0441979.  
 XX  
 PA (SELE-) SELECTIVE GENETICS INC.  
 XX  
 PI Chandler LA, Sosnowski BA, Baird JA;  
 XX  
 DR WPI: 2000-292008/25.  
 DR P-PSDB; AAY90402.  
 XX  
 PT Gene delivery system, useful for treating or preventing cancer and  
 PT rheumatoid arthritis, comprises receptor-internalized ligand linked to  
 PT nucleic acid binding domain and nucleic acid  
 XX  
 PS Disclosure: Columns 83-84; 131pp; English.  
 XX  
 CC The invention relates to a novel gene delivery composition for the  
 CC targeted delivery of cytotoxins or prodrug-converting enzymes to  
 CC proliferating cells. The gene delivery composition comprises a protein  
 CC that binds the fibroblast growth factor receptor (FGFR) which is fused  
 CC or chemically conjugated to a nucleic acid binding domain. The nucleic  
 CC acid binding domain is complexed with a suitable expression construct  
 CC encoding a cytotoxin such as saporin. One or more linkers may join the  
 CC FGFR-binding protein to the nucleic acid binding protein. These are  
 CC selected to increase the specificity, toxicity, solubility, serum  
 CC stability or intracellular availability, and may serve to promote  
 CC condensation of nucleic acids for delivery to a cell. The fusion protein  
 CC binds to FGFR and is internalised by cells that carry this receptor. The  
 CC gene delivery composition is used for the therapeutic alteration of the  
 CC function, gene expression and viability of cells. In particular, it may  
 CC be used for the treatment and prevention of cell proliferative  
 CC disorders, for example after eye surgery, melanoma and many other sorts  
 CC of cancer, rheumatoid arthritis, restenosis, Dupuytren's contracture,  
 CC diabetic retinopathy, psoriasis and eczema. The gene delivery  
 CC compositions of the invention have high specificity for particular cells  
 CC and can deliver larger amounts of DNA compared to prior art methods.  
 CC Sequences AAA12853- AAA12856 represent cDNA clones encoding vascular  
 CC endothelial growth factor (VEGF), and sequences AAY90402-Y90405 represent  
 CC the encoded VEGF proteins. AAA12857 represents cDNA encoding human  
 CC heparin-binding epidermal growth factor (HBEGF) precursor, and  
 CC AAY90406-Y90409 represent HBEGF precursor and mature proteins.  
 XX

SQ Sequence 473 BP; 131 A; 119 C; 130 G; 93 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 1,93e-87 Length: 473  
 Score: 792.00 Matches: 141  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 21 Gaps: 0  
 US-09-884-050-2 (1-141) x AAA12853 (1-473)  
 QY 1 MetAsnPhelLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuLeuTyrLeuHisHis 20  
 Db 13 ATCAACTTTCTGCTGCTTGGTGCATTTGGAGCCTTGCCTTGTGCTTACCTCCACCAT 72  
 QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluVal 40  
 Db 73 GCCAAGTGTGTCCTCCAGGCTGCCACCCATGGCAGAGGAGGAGGAGGAGGAGGAGGAGG 132  
 QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
 Db 133 GTCAAGTTTCATGATGCTATCAGCGCAGCTACTGCCATCCTCAGAGACCTGGTGGAC 192  
 QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
 Db 193 ATCTTCCAGGAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 252  
 QY 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
 Db 253 ATCGATGCGGGGGGCTGCTCAATGACGAGGCGCTGGAGTGTGCCCCATGAGGAGTCC 312  
 QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
 Db 313 AACATCACCATGCGAGATTATGCGGATCAACCTCACCAAGCCACATAGGAGAGATG 372  
 QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
 Db 373 AGCTTCTCAGCAGCAACAATGTGAATGCGAGCACAAGAAAGATAGAGCAAGACAAAGAA 432  
 QY 141 Lys 141  
 Db 433 AAA 435  
 RESULT 10  
 AAZ29996  
 ID AAZ29996 standard; cDNA; 495 BP.  
 XX  
 AC AAZ29996;  
 XX  
 DT 26-JAN-2000 (first entry)  
 XX  
 DE Nucleotide sequence of VEGF-A138 protein coding region.  
 XX  
 KW Vascular endothelial factor; VEGF; VEGF-A138; variant; vascular disease;  
 KW cardiovascular disease; vascular cell proliferation; angioplasty;  
 KW restenosis; drug permeation; tumour; ischemic condition;  
 KW cardiac infarction; chronic coronary ischemia; stroke; wound treatment;  
 KW chronic lower limb ischemia; peripheral vascular disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 XX 1..495  
 CDS /\*tag= a  
 FT /product= "VEGF-A138"  
 FT 1..78  
 FT sig\_peptide /\*tag= b  
 FT /note= "secretion signal sequence"  
 FT 1..90  
 FT exon /\*tag= c  
 FT /number= 1  
 FT 91..118  
 FT exon



FT /\*tag= d  
 FT /number= 2  
 FT exon 119..315  
 FT /\*tag= e  
 FT /number= 3  
 FT exon 316..392  
 FT /\*tag= f  
 FT /number= 4  
 FT exon 393..422  
 FT /\*tag= g  
 FT /number= 5  
 FT exon 423..465  
 FT /\*tag= h  
 FT /number= 6b  
 FT exon 467..492  
 FT /\*tag= i  
 FT /number= 8  
 PN WO9940197-A2.  
 XX  
 PD 12-AUG-1999.  
 XX  
 PF 04-FEB-1999; 99WO-US02425.  
 XX  
 PF 06-FEB-1998; 98US-0073979.  
 PR  
 PA (COLL-) COLLATERAL THERAPEUTICS INC.  
 XX  
 PI Baird A, Andreason G;  
 XX  
 DR WPI: 1999-600967/51.  
 DR P-PSDB; AAY43482.  
 XX  
 XX New growth factor variants, useful for treating cardiovascular disease,  
 PT especially by stimulating vascular cell proliferation -  
 XX  
 PS Claim 19; Fig 3; 101pp; English.  
 XX

CC The present sequence encodes vascular endothelial factor VEGF-A138.  
 CC It is a VEGF-A variant of the invention. The specification describes new  
 CC VEGF-A variants in which exon 6a is excluded (other forms which contain  
 CC both exon 6a and 6b are also described). The variants have a modified  
 CC affinity for matrix and low affinity receptors. This alters the  
 CC bioavailability of the proteins when administered directly to cells.  
 CC These variants are used to treat vascular disease, especially  
 CC cardiovascular disease, by stimulating vascular cell proliferation. They  
 CC enhance epithelialisation of diseased vessels, especially after  
 CC angioplasty. The re-endothelialisation reduces or prevents restenosis.  
 CC They are also useful for enhancing drug permeation by tumours and for  
 CC treating ischemic conditions such as cardiac infarction, chronic coronary  
 CC ischemia, chronic lower limb ischemia, stroke and peripheral vascular  
 CC disease. In addition they may be used to treat wounds.  
 XX

SQ Sequence 495 BP; 126 A; 133 C; 136 G; 100 T; 0 other;

Alignment Scores:  
 Pred. No.: 2,03e-87 Length: 495  
 Score: 792.00 Matches: 141  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-09-884-050-2 (1-141) x AA229996 (1-495)

Oy 1 MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrlleuHis 20  
 Db 1 ATGAATCTCTCTCTCTGGTGATGGAGCCCTTGCTGCTCTACTCCACCAT 60  
 Oy 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlyGlnAsnHisGluVal 40  
 Db 61 GCCAAGTGTCCCGCTGCACCCATGGCAGNAGAGGAGGAGGAGCAATCATCAGCAAGTG 120

Oy 41 VallysPheMetAspValTyrlleGlnArgSerTyrlleCysHisProIleGluThrLeuValAsp 60  
 Db 121 GTGAAGTTTCATGGATGTCTATCAGCGCAGCTACTGCCATCCAAATGAGACCTGGTGAC 180  
 Oy 61 IlePheGlnGluTyrlleProAspGluIleGluTyrllePheLysProSerCysValProLeu 80  
 Db 181 ATCTTCCAGGAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
 Oy 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
 Db 241 ATGGGATCGGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTGCCCTCCTGAGGAGTCC 300  
 Oy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
 Db 301 AACATCACCATGCAGATTATCGGATCAAACTCACCAGGCCAGCACATAGGAGAGATG 360  
 Oy 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
 Db 361 AGTTCTCTACAGCACACAAATGTGATGATGATGATGATGATGATGATGATGATGATGATG 420  
 Oy 141 Lys 141  
 Db 421 AAG 423  
 RESULT 11  
 AAV28396  
 ID AAV28396 standard; cDNA; 516 BP.  
 XX AC AAV28396;  
 XX DT 24-JUL-1998 (first entry)  
 DE Vascular endothelial growth factor-145 (VEGF145) encoding cDNA.  
 XX KW Vascular endothelial growth factor; VEGF145; angiogenic factor;  
 XX KW cell proliferation; cardiovascular disease; drug permeation; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 79..516  
 FT /\*tag= a  
 FT /transl\_except= (pos: 457..459, aa: Arg)  
 FT sig\_peptide 1..78  
 FT /\*tag= b  
 FT mat\_peptide 79..514  
 FT /\*tag= c  
 PN WO9810071-A1.  
 XX 12-MAR-1998.  
 PD 04-SEP-1997; 97WO-US15471.  
 PF 21-JAN-1997; 97US-0784551.  
 PR 06-SEP-1996; 96US-0025537.  
 XX (COLL-) COLLATERAL THERAPEUTICS.  
 XX (TECR) TECHNION RES & DEV CO LTD.  
 PI Keshet E, Neufeld G, Poltorak Z, Vladavsky I;  
 XX WPI: 1998-193621/17.  
 DR P-PSDB; AAW56693.  
 XX Vascular endothelial growth factor-145 splice variant - useful as an  
 PT angiogenic factor for treatment of cardiovascular disease  
 XX Claim 14; Fig 2; 73pp; English.  
 XX This cDNA encodes a vascular endothelial growth factor-145 (VEGF145)  
 CC which is used to stimulate vascular cell proliferation. Polynucleotides  
 CC encoding VEGF145 are useful for treatment of cardiovascular or vascular

CC disease in mammals, especially humans. They are also useful for enhancing  
 CC drug permeation by tumours. VEGF145 can also be administered to stimulate  
 CC vascular cell proliferation or to enhance endothelialization of diseased  
 CC vessels (especially re-endothelialization after angioplasty) in mammals.  
 CC VEGF145, which binds as weakly as VEGF165 to heparin, binds much better  
 CC than VEGF165 to the extracellular matrix (ECM). However, unlike VEGF189,  
 CC VEGF145 is secreted from producer cells and binds efficiently to ECM.  
 CC This combination of properties render VEGF145 the only known VEGF variant  
 CC that is secreted from producing cells retaining at the same time ECM  
 CC binding properties. This makes VEGF145 likely to diffuse towards the  
 CC target blood vessels, while some of the produced VEGF145 will be retained  
 CC by ECM components along the path of diffusion. This ECM bound pool will  
 CC dissociate slowly allowing a longer period of activity. Additionally, the  
 CC biological activity of VEGF145 is protected against oxidative damage  
 CC unlike VEGF forms such as VEGF121 thereby giving it a longer half-life.  
 XX  
 SQ Sequence 516 BP; 150 A; 125 C; 144 G; 97 T; 0 other;

Alignment Scores: 2.17e-87 Length: 516  
 Pred. No.: 792.00 Matches: 141  
 Score: 792.00  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 19 Gaps: 0

US-09-884-050-2 (1-141) x AAV28396 (1-516)

QY 1 MetAsnPhelLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20  
 DB 1 ATGAACCTTCTGCTGCTTGGGTGCATTGGAGCCTTGCCCTTGCTCTACCTCCACCAT 60  
 QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40  
 DB 61 GCCAAGTGTGCCAGCTGCACCCATGGCAGAGGAGGAGGAGGAGATCATCATCAGAGTG 120  
 QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
 DB 121 GTCAAGTTCATGATGTCTATCAGCGCAGCTACTGCCATCCATCGAGACCTGGTGGAC 180  
 QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
 DB 181 ATCTTCAGAGTACCTGTATGATGATCGATCATCTTCAAGCCATCCTGTGCCCTCG 240  
 QY 81 MetArgCysGlyGlyCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
 DB 241 ATCGGATGCGGGGCTGCTCATATGACGAGGCGCTGGAGTGTGTGCCCTGAGGAGTCC 300  
 QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
 DB 301 AACATCACCATGCAGATTATGCGGATCAAAACCTCACCAAGGCCACATAGGAGATG 360  
 QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
 DB 361 AGTTCTCTACGACACACAAATATGATGATGAGACCAACCAAGAAAGATAGAGCAAGAA 420  
 QY 141 Lys 141  
 DB 421 AAA 423

RESULT 12  
 AAX57724  
 ID AAX57724 standard; cDNA; 516 BP.

XX  
 AC AAX57724;  
 XX  
 DT 03-AUG-1999 (first entry)  
 XX  
 DE Human VEGF(145) coding sequence.

XX Human; vascular endothelial growth factor; VEGF; vector; stimulation;  
 KW angiogenesis; mammal; peripheral; cardiac; tissue; ischaemia; perfusion;  
 KW neovascularisation; muscle; ss.

XX Homo sapiens.  
 OS  
 FH Key.  
 FT CDS Location/Qualifiers  
 FT 1..516  
 FT /\*tag= a  
 FT /product= "human VEGF(145)"  
 FT 1..78  
 FT /\*tag= b  
 FT 78..516  
 FT /\*tag= c  
 FT mat\_peptide  
 FT  
 XX WO9921590-A1.  
 PN  
 PD 06-MAY-1999.  
 XX  
 PF 23-OCT-1998; 98WO-US22668.  
 XX  
 PR 26-NOV-1997; 97GB-0024906.  
 PR 27-OCT-1997; 97US-0063629.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Bett AJ, Huckle WR, Kendall RL, Thomas KA;  
 DR WPI; 1999-302907/25.  
 DR P-PSDB; AAY07473.  
 XX  
 PT Stimulating angiogenesis by expressing vascular endothelial growth  
 PT factor  
 PS Example 1; Fig 1; 46pp; English.  
 CC This sequence represents the coding sequence for the 145 amino acid form  
 CC of human vascular endothelial growth factor (VEGF(145)), which, when  
 CC administered in a vector, can be used to stimulate angiogenesis in a  
 CC mammal. Administration of the VEGF(145) is used to treat peripheral,  
 CC cardiac or other tissue ischaemias, i.e. to increase neovascularisation,  
 CC perfusion and performance of ischaemic muscle.  
 XX  
 SQ Sequence 516 BP; 150 A; 126 C; 143 G; 97 T; 0 other;  
 Alignment Scores: 2.17e-87 Length: 516  
 Pred. No.: 792.00 Matches: 141  
 Score: 792.00  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 20 Gaps: 0  
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 QY 1 MetAsnPhelLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20  
 DB 1 ATGAACCTTCTGCTGCTTGGGTGCATTGGAGCCTTGCCCTTGCTCTACCTCCACCAT 60  
 QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40  
 DB 61 GCCAAGTGTGCCAGCTGCACCCATGGCAGAGGAGGAGGAGGAGATCATCATCAGAGTG 120  
 QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
 DB 121 GTCAAGTTCATGATGTCTATCAGCGCAGCTACTGCCATCCATCGAGACCTGGTGGAC 180  
 QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
 DB 181 ATCTTCAGAGTACCTGTATGATGATCGATCATCTTCAAGCCATCCTGTGTGCCCTCG 240  
 QY 81 MetArgCysGlyGlyCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
 DB 241 ATCGGATGCGGGGCTGCTCATATGACGAGGCGCTGGAGTGTGTGCCCTGAGGAGTCC 300  
 QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120

```
|||||
Db 301 AACATCACCATGCAGATTATGCGGATCAAACTCACCAGGCCAGCACATAGGAGATG 360
QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140
Db 361 AGCTTCTTACAGCACAAATGTGAATGCGAGACCAAGAAAGATAGCAAGCAAGAA 420
QY 141 Lys 141
|||
Db 421 AAA 423

RESULT 13
AAH21876
ID AAH21876 standard; cDNA; 544 BP.
XX
AC AAH21876;
XX
DT 16-AUG-2001 (first entry)
DE Human VEGF splice variant VEGF121 encoding cDNA SEQ ID NO:3.
XX
KW Human; vascular endothelial growth factor; VEGF splice variant; VEGF;
KW VEGF121; colon cancer cell line acquired malignancy; anticancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 9..452
FT /tag= a
FT sig_peptide /product= "VEGF splice variant VEGF121"
FT 9..86
FT /tag= b
FT mat_peptide 87..449
FT /tag= c
XX
XX JP2001061483-A.
XX
XX 13-MAR-2001.
XX
XX 31-AUG-1999; 99JP-0244198.
XX
XX 31-AUG-1999; 99JP-0244198.
XX
XX (EISA ) EISAI CO LTD.
XX
XX WPI: 2001-294711/31.
XX P-PSDB: AAB98080.
XX
XX Human colon cancer cell line is transfected with VEGF gene and selected
XX for having acquired malignancy -
XX
XX Example 1; Page 6; 8pp; Japanese.
XX
CC The present invention describes a method in which the vascular
CC endothelial growth cell (VEGF) gene is introduced to a human colon
CC cancer cell showing no malignancy, and a cell line highly expressing
CC VEGF is selected to get a cell line acquired malignancy. Also described
CC are: (1) a human colon cancer cell line acquired malignancy by the above
CC method; (2) WiDr cell line acquired malignancy by the above method;
CC (3) a method for screening an anticancer agent by using the above human
CC colon cancer cell line, preferably WiDr cell line, acquired malignancy;
CC and (4) a compound screened by the above method. The human colon cancer
CC cell line acquired malignancy can be used for screening an anticancer
CC agent. The present sequence encodes the human VEGF splice variant
CC VEGF121, which is used in an example from the present invention.
XX
SQ Sequence 544 BP; 150 A; 141 C; 150 G; 103 T; 0 other;

Alignment Scores:
Pred. No.: 2,33e-87 Length: 544
Score: 792.00 Matches: 141
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
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QY 1 MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyLeuHisHis 20
Db 9 ATGAACCTTCTGCTGTCTGGTGCATTGGAGCCCTTGCTTGTGCTTACCTCAGCAT 68
QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluVal 40
Db 69 GCCAAGTGGTCCCGAGCTGCACCATGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 128
QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60
Db 129 GTGAAGTTCATGGATGTCTATCAGCGCAGCTACTGCCATCAATCGAGACCTCGTGGAC 188
QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80
Db 189 ATCTTCCAGGAGTACCTGTATGATGAGATGAGTACATCTTCAAGCCATCCTGTGCCCCGTG 248
QY 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100
Db 249 ATGCGATGCGGGGGCTGCTGCATGACGAGGGGCTGGAGTGTGCCCCACTGAGGAGTCC 308
QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120
Db 309 AACATCACCATGCAGATTATGCGGATCAAACTCACCAGGCCAGCACATAGGAGATG 368
QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140
Db 369 AGCTTCTTACAGCACAAATGTGAATGCGAGACCAAGAAAGATAGCAAGCAAGAA 428
QY 141 Lys 141
|||
Db 429 AAA 431

RESULT 14
AAZ29999
ID AAZ29999 standard; DNA; 545 BP.
XX
AC AAZ29999;
XX
XX 26-JAN-2000 (first entry)
XX
XX Nucleotide sequence of VEGF-A145.
XX
KW Vascular endothelial factor; VEGF; VEGF-A145; variant; vascular disease;
KW cardiovascular disease; vascular cell proliferation; angioplasty;
KW restenosis; drug permeation; tumour; ischemic condition;
KW cardiac infarction; chronic coronary ischemia; stroke; wound treatment;
KW chronic lower limb ischemia; peripheral vascular disease; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO9940197-A2.
XX
XX 12-AUG-1999.
XX
XX 04-FEB-1999; 99WO-US02425.
XX
XX 06-FEB-1998; 98US-0073979.
XX
XX (COLL-) COLLATERAL THERAPEUTICS INC.
XX
XX Baird A, Andreason G;
XX
XX WPI: 1999-600967/51.
XX
XX New growth factor variants, useful for treating cardiovascular disease,
XX especially by stimulating vascular cell proliferation -
XX
XX Example 1; Page 70; 101pp; English.
```



QY 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
|||||  
Db 241 ATCGATCGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGTGCCCACTGAGGAGTCC 300  
|||||  
QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
|||||  
Db 301 AACATCACCATGCGAGATTATGCGGATCAAACTCACCAGGCCAGCACATAGGAGAGATG 360  
|||||  
QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
|||||  
Db 361 AGCTTCCTACAGCACACAAATGTGATGCAGACCAAGAAAGATAGAGCAAGACAGAA 420  
|||||  
QY 141 Lys 141  
|||  
Db 421 AAA 423

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GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

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Title: US-09-884-050-2

Perfect score: 792

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Post-processing: Minimum Match 0%

Maximum Match 100%

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13: gb\_un:\*  
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16: em\_fun:\*  
17: em\_hum:\*  
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19: em\_mu:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	792	100.0	444	6	AR198591	1	AR198591 Sequence
3	792	100.0	444	6	AX048686	1	AX048686 Sequence
4	792	100.0	444	6	AX050391	1	AX050391 Sequence
5	792	100.0	444	9	AF214570	1	AF214570 Homo sapi
6	792	100.0	516	6	AX029451	1	AX029451 Sequence
7	792	100.0	544	6	E49139	1	E49139 Human large
8	792	100.0	573	6	A92244	1	A92244 Sequence 3
9	792	100.0	630	9	HS010438	1	HS010438 Homo sapi
10	792	100.0	642	6	AR198594	1	AR198594 Sequence
11	792	100.0	642	6	AX050397	1	AX050397 Sequence
12	792	100.0	645	6	A92246	1	A92246 Sequence 5
13	792	100.0	648	6	AR117116	1	AR117116 Sequence
14	792	100.0	696	6	A92248	1	A92248 Sequence 7
15	792	100.0	699	6	AR198595	1	AR198595 Sequence
16	792	100.0	699	6	AX050399	1	AX050399 Sequence
17	792	100.0	774	6	AR118875	1	AR118875 Sequence
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19	792	100.0	774	6	E13215	1	E13215 Human mRNA
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21	792	100.0	774	6	E14233	1	E14233 Human mRNA
22	792	100.0	774	6	E15156	1	E15156 Human VEGF
23	792	100.0	815	6	AX234496	1	AX234496 Sequence
24	792	100.0	815	9	S85192	1	S85192 Homo sapien
25	792	100.0	1195	9	HUMVEF	1	HUMVEF Human vascu
26	792	100.0	1873	6	E15157	1	E15157 Human VEGF
27	792	100.0	1873	6	E22645	1	E22645 Antisense n
28	787	99.4	541	6	AX204783	1	AX204783 Sequence
29	787	99.4	541	9	AF091352	1	AF091352 Homo sapi
30	787	99.4	573	6	AX060342	1	AX060342 Sequence
31	787	99.4	576	6	AR198593	1	AR198593 Sequence
32	787	99.4	576	6	AX050395	1	AX050395 Sequence
33	787	99.4	576	6	AX481507	1	AX481507 Sequence
34	787	99.4	576	9	AB021221	1	AB021221 Homo sapi
35	787	99.4	576	9	AF486837	1	AF486837 Homo sapi
36	787	99.4	576	9	S82167	1	S82167 simVEGF165-
37	787	99.4	606	9	AF430806	1	AF430806 Homo sapi
38	787	99.4	640	9	AY047581	1	AY047581 Homo sapi
39	787	99.4	649	9	HSVEGF	1	HSVEGF H.sapiens v
40	787	99.4	990	6	AX039419	1	AX039419 Sequence
41	787	99.4	990	6	AX135799	1	AX135799 Sequence
42	787	99.4	990	6	AX234351	1	AX234351 Sequence
43	787	99.4	990	6	AX409689	1	AX409689 Sequence
44	787	99.4	990	6	BD006221	1	BD006221 Variants
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ALIGNMENTS

RESULT 1

A92242  
LOCUS A92242 441 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 1 from Patent WO9820027.  
ACCESSION A92242  
VERSION A92242.1 GI:6741017  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 441)  
AUTHORS Ylae-Herttua, S. and Martin, J.F.  
TITLE THERAPEUTIC USE OF GROWTH FACTOR, AND DELIVERY DEVICE, ESPECIALLY FOR THE TREATMENT OF INTIMAL HYPERPLASIA  
JOURNAL Patent: WO 9820027-A 1 14-MAY-1998  
FEATURES  
source location/Qualifiers  
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BASE COUNT 120 a 113 c 122 g 86 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 9.97e-86 Length: 441  
Score: 792.00 Matches: 141  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-884-050-2 (1-141) x A92242 (1-441)  
QY 1 MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20  
Db 1 ATGAACCTTTCTGCTGCTTGGTGTCATTGGAGCCTTGCCTTGCTCTACCTCCACCAT 60  
QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40  
Db 61 GCCAAGTGTCTCCAGGCTGCACCCATGGCAGAGGAGGAGGAGGAGATCATCAGGAATG 120  
QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
Db 121 GTCAAGTTCATGATGCTATATCAGCGCAGCTACTGCCATCCATCAGACCTTGGTGAC 180  
QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
Db 181 ATCTTCAGAGGATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
QY 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
Db 241 ATCCGATGCGGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCTCCACTGAGGAGTCC 300  
QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
Db 301 AACATCACCATGAGATTTATGCGGATCAACCTCACCAGGCCAGCACATAGGAGATG 360  
QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
Db 361 AGCTTCCTACAGCACACAATAATGTGAATGCAGACCAACAAAGAAAGATAGAGCAAGCAAG 420  
QY 141 Lys 141  
Db 421 AAA 423  
RESULT 2

AR198591  
LOCUS AR198591 444 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 6 from patent US 6352975.  
ACCESSION AR198591  
VERSION AR198591.1 GI:20248440  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 444)  
AUTHORS Schreiner, G.F. and Johnson, R.J.  
TITLE Methods of treating hypertension and compositions for use therein  
JOURNAL Patent: US 6352975-A 6 05-MAR-2002  
FEATURES  
source location/Qualifiers  
1..444 /organism="unknown"  
BASE COUNT 121 a 113 c 122 g 88 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 1e-85 Length: 444  
Score: 792.00 Matches: 141  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-884-050-2 (1-141) x AR198591 (1-444)  
QY 1 MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20  
Db 1 ATGAACCTTTCTGCTGCTTGGTGTCATTGGAGCCTTGCCTTGCTCTACCTCCACCAT 60  
QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40  
Db 61 GCCAAGTGTCTCCAGGCTGCACCCATGGCAGAGGAGGAGGAGGAGATCATCAGGAATG 120  
QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
Db 121 GTCAAGTTCATGATGCTATATCAGCGCAGCTACTGCCATCCATCAGACCTTGGTGAC 180  
QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
Db 181 ATCTTCAGAGGATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
QY 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
Db 241 ATCCGATGCGGGGGCTGCTGCAATGACGAGGCGCTGGAGTGTGCTCCACTGAGGAGTCC 300  
QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
Db 301 AACATCACCATGAGATTTATGCGGATCAACCTCACCAGGCCAGCACATAGGAGATG 360  
QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
Db 361 AGCTTCCTACAGCACACAATAATGTGAATGCAGACCAACAAAGAAAGATAGAGCAAGCAAG 420  
QY 141 Lys 141  
Db 421 AAA 423  
RESULT 3  
LOCUS AX048686 444 bp DNA linear PAT 12-JAN-2001  
DEFINITION Sequence 3 from Patent WO0071716.  
ACCESSION AX048686  
VERSION AX048686.1 GI:12225840  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 444)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.



US-09-884-050-2 (1-141) x AX050391 (1-444)

RESULT	5
AF214570	
LOCUS	444 bp mRNA linear PRI 23-DEC-1999
DEFINITION	Homo sapiens vascular endothelial growth factor isoform l2l precursor, mRNA, complete cds.
ACCESSION	AF214570
VERSION	AF214570.1 GI:6631028
KEYWORDS	.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



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Sequence 3 from Patent WO9820027.
A92244
A92244.1  GI:6741019
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unidentified.
unidentified
unclassified.
unclassified.
REFERENCE 1 (bases 1 to 573)
AUTHORS Ylae-Herttuala, S. and Martin, J. F.
TITLE THERAPEUTIC USE OF GROWTH FACTOR, AND DELIVERY DEVICE, ESPECIALLY
FOR THE TREATMENT OF INTIMAL HYPERPLASIA
JOURNAL Patent: WO 9820027-A 3 14-MAY-1998.
YLAE HERTTUALA SEPO (FI); MARTIN JOHN FRANCIS (GB)
FEATURES
source Location/Qualifiers
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1. .>573
CDS

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BASE COUNT	157 a 143 c 158 g 115 t
ORIGIN	
Alignment Scores:	
Pred. No.:	1,36e-85
Score:	792.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
Mismatches:	0
Indels:	0
Conservative:	0
Matches:	141
Length:	573

DB:	6	gaps:	0
US-09-884-050-2 (1-141) x A92244 (1-573)			
Qy	1	MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuLeuLeuLeuHis	20
Db	1	ATGAACTTTCTGCTGTCTTGGGTGCATTGGAGCTCGCCTTGCTGCTACCTCCACCAT	60
Qy	21	AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluVal	40
Db	61	GCCAAAGTGGTCCCAGGCTGCACCCATGGCAAGAGGAGGGCGAGAATCATCAGGAAGTG	120
Qy	41	VallysPheMetAspValTyrglnArgSerTyrCysHisProIleGluThrLeuValAsp	60
Db	121	GTGAAGTTTCATGGATGCTATCAGCGCAGCTACTGCCATCCAATCGAGACCTGGTGGAC	180
Qy	61	IlePheGlnGluTyrrProAspGluIleelutrrIlePheLysProSerCysValProLeu	80
Db	181	ATCTTCCAGGAGTAGTACCCTGTATGAGATCGAGTACATCTTCAAGCCATCTGTGTGCCGCTG	240
Qy	81	MetArgCysGlyGlyCysCysAsnAspGluLeuGluCysValProThrGluGluSer	100
Db	241	ATGCGATGCGGGGGCTGCTGCAATGACGAGGGCTGGAGTGTGTGCCACATGAGGAGTCC	300
Qy	101	AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet	120
Db	301	AACATCACCATGCAGATATGCGGATCAACCTCACCAGGCCAGCAGCATAGGAGAGATG	360
Qy	121	SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu	140
Db	361	AGCTTCTTACAGCACAAACAAATGTGAATGCAGACCAAGAAAGATAGACGAAGACAAGA	420
Qy	141	Lys 141	
Db	421	AAA 423	
RESULT	9		
HS	A010438		

\*\*\*\*\*

LOCUS HSA010438 630 bp mRNA linear PRI 15-JAN-1999  
DEFINITION Homo sapiens mRNA for vascular endothelial growth factor, splicing  
variant VEGF183.  
ACCESSION AJ010438  
VERSION AJ010438.1 GI:3647280  
KEYWORDS vascular endothelial growth factor; vegf gene; VEGF183 protein.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 630)  
AUTHORS Lei, J., Jiang, A. and Pei, D.  
TITLE Direct Submission\*  
JOURNAL Submitted (20-AUG-1998) Pei D., Pharmacology, University of  
Minnesota, 3-249 Millard Hall, 435 Delaware St. S.E., Minneapolis,  
MN55455, USA  
REFERENCE 2 (bases 1 to 630)  
AUTHORS Lei, J., Jiang, A. and Pei, D.  
TITLE Identification and characterization of a new splicing variant of  
vascular endothelial growth factor: VEGF183  
JOURNAL Biochim. Biophys. Acta 1443 (3), 400-406 (1998)  
MEDLINE 99096474  
PUBMED 9878851  
FEATURES  
source Location/Qualifiers  
1..630 /organism="Homo sapiens"  
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1..630 /gene="vegf"  
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mat\_peptide 79..627 /gene="vegf"  
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Alignment Scores: 1.52e-85 Length: 630  
Pred. No.: 792.00 Matches: 141  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 9 Gaps: 0  
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QY 1 MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20  
Db 1 ATGAACCTTCTGCTGTGGTGGTATGGAGCCTTGGCTTGTCTACCTCCACCAT 60  
QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40  
Db 61 GCCAAGTGGTCCAGGCTGCCATGGCAGAGAGAGAGAGAGAGAGATCATCAGAGTG 120  
QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
Db 121 GTGAAGTTTCATGATGCTATCAGCCAGCTACTGCGATCCCAATCGAGACCTTGGTGGAC 180  
QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
Db 181 ATCTCCAGAGTACCTGATGAGATGAGTACATCTTCAAGCCATCTCTGTGTGCCCTG 240  
QY 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
Db 241 ATCGCATCGGGGGCTGCTGCAATGACGAGGGCTGTGAGTGTGTGCCACTGAGGAGTCC 300  
QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
Db 301 AACATCACCATGAGATTATCGGATCAAACTCACCAGCCAGCAGATAGAGAGATG 360

QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
Db 181 ATCTCCAGAGTACCTGATGAGATGAGTACATCTTCAAGCCATCTCTGTGTGCCCTG 240  
QY 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
Db 241 ATCGCATCGGGGGCTGCTGCAATGACGAGGGCTGTGAGTGTGTGCCACTGAGGAGTCC 300  
QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
Db 301 AACATCACCATGAGATTATCGGATCAAACTCACCAGCCAGCAGATAGAGAGATG 360  
QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
Db 361 AGCTTCCTACAGCACACAATGTGAATGCAGACCAAGAAGATAGAGCAAGAAGAA 420  
QY 141 Lys 141  
Db 421 AAA 423  
RESULT 10  
LOCUS AR198594  
DEFINITION Sequence 9 from patent US 6352975.  
ACCESSION AR198594  
VERSION AR198594.1 GI:20248443  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 642)  
AUTHORS Schreiner, G.F. and Johnson, R.J.  
TITLE Methods of treating hypertension and compositions for use therein  
JOURNAL Patent: US 6352975-A 9 05-MAR-2002;  
FEATURES  
source Location/Qualifiers  
1..642 /organism="unknown"  
BASE COUNT 186 a 153 c 180 g 123 t  
ORIGIN  
Alignment Scores: 1.56e-85 Length: 642  
Pred. No.: 792.00 Matches: 141  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 6 Gaps: 0  
DB:  
US-09-884-050-2 (1-141) x AR198594 (1-642)  
QY 1 MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20  
Db 1 ATGAACCTTCTGCTGTGGTGGTATGGAGCCTTGGCTTGTCTACCTCCACCAT 60  
QY 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40  
Db 61 GCCAAGTGGTCCAGGCTGCCATGGCAGAGAGAGAGAGAGAGATCATCAGAGTG 120  
QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
Db 121 GTGAAGTTTCATGATGCTATCAGCCAGCTACTGCGATCCCAATCGAGACCTTGGTGGAC 180  
QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
Db 181 ATCTCCAGAGTACCTGATGAGATGAGTACATCTTCAAGCCATCTCTGTGTGCCCTG 240  
QY 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
Db 241 ATCGCATCGGGGGCTGCTGCAATGACGAGGGCTGTGAGTGTGTGCCACTGAGGAGTCC 300  
QY 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
Db 301 AACATCACCATGAGATTATCGGATCAAACTCACCAGCCAGCAGATAGAGAGATG 360

Db	301	AAATCATCAGTGCAGATTATGCGGATCAAACTCACCAAGGCCACACATAGGAGAGATG	360
Qy	121	SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaAaArgGlnGlu	140
Db	361	AGCTTCCTACAGCACAAATAATGTGAATGCAGACCAAGAAAGATAGACGAACAGAA	420
Qy	141	Lys 141	
Db	421	AAA 423	
RESULT	12		
LOCUS	A92246		
DEFINITION	Sequence 5 from Patent WO9820027.	645 bp	DNA
ACCESSION	A92246		linear
VERSION	A92246.1	GI:6741021	PAT 22-JAN-2000
KEYWORDS	unidentified.		
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 645)		
AUTHORS	Ylae-Herttuala, S. and Martin, J.F.		
TITLE	THERAPEUTIC USE OF GROWTH FACTOR, AND DELIVERY DEVICE, ESPECIALLY FOR THE TREATMENT OF INTIMAL HYPERPLASIA		
JOURNAL	Patent: WO 9820027-A 5 14-MAY-1998;		
FEATURES	YLAE HERTTUALA SEPO (FI); MARTIN JOHN FRANCIS (GB)		
source	Location/Qualifiers		
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BASE COUNT	185 a 155 c 181 g 124 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	1.57e-85	Length:	645
Score:	792.00	Matches:	141
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-09-884-050-2 (1-141) x A92246 (1-645)			
Qy	1	MetAsnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuLeuTyrLeuHisHis	20
Db	1	ATGAACATTCTGCTGTCTTGGGTGCATTTGGAGCCTCGCTTGTCTACCTCCACAT	60
Qy	21	AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlyGlnAsnHisHisGluVal	40
Db	61	GCCAAGTGTGTCACAGCTGCACCCATGCACAGAGAGAGGGCAGAAATCATCAACAAGT	120
Qy	41	ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp	60
Db	121	GTGAAGTTCATGGATGCTATCACGCGCAGCTACTGCCATCAATCGAGACCTCGTGGAC	180
Qy	61	IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu	80
Db	181	ATCTTCCAGGAGTAGTACCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCGCT	240
Qy	81	MetArgCysGlyGlyCysCysAsnAspGluClyLeuGluCysValProThrGluGluSer	100
Db	241	ATGCGATGCGGGGGCTGCTGCAATGACGAGGGCTGGAGTGTGGCCACTGAGAGATCC	300
Qy	101	AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet	120

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Db 301 AACATCACCATGAGATTATGCGGATCAAAACCTCACCAGGCCAGCACATAGAGAGATG 360  
Qy 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
|||||  
Db 361 AGCTTCCTACGACACAAACAAATGTAATGAGACCAACAAAGAGATAGAGCAAGACAA 420  
Qy 141 Lys 141  
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Db 421 AAA 423  
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RESULT 13  
AR117116  
LOCUS AR117116 648 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 48 from patent US 6140073.  
ACCESSION AR117116  
VERSION AR117116.1 GI:14098022  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 648)  
AUTHORS Bayne, M.L. and Thomas, K.A. Jr.  
TITLE Vascular endothelial cell growth factor C subunit  
JOURNAL Patent: US 6140073-A 48 31-OCT-2000;  
FEATURES  
Location/Qualifiers  
source  
BASE COUNT 186 a 155 c 180 g 127 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1-57e-85 Length: 648  
Score: 792.00 Matches: 141  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-884-050-2 (1-141) x AR117116 (1-648)

Qy 1 MetaSnPheLeuLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20  
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Db 1 ATGAACCTTCTGCTGCTGGTGCTATGGAGCCTTGCCTTGCTGCTACCTCCACCAT 60  
Qy 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluVal 40  
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Db 61 GCCAAGTGGTCCAGGCTGCACCATGGCAGAGAGAGAGGCGCAGATCATCAGAAAGTG 120  
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Db 121 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCAATCGAGACCTCGTGGAC 180  
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Db 241 ATGCGATGCGGGGGCTGCTGCAATGACAGAGGCGCTGGAGTGTGCCCCACTGAGAGTCC 300  
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Db 361 AGCTTCCTACGACACAAACAAATGTAATGACAGACCAACAAAGAGATAGAGCAAGACAA 420  
Qy 141 Lys 141  
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Db 421 AAA 423  
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DEFINITION Sequence 7 from Patent WO9820027.  
ACCESSION A92248  
VERSION A92248.1 GI:6741023  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 696)  
AUTHORS Ylae-Herttuala, S. and Martin, J.F.  
TITLE THERAPEUTIC USE OF GROWTH FACTOR, AND DELIVERY DEVICE, ESPECIALLY  
FOR THE TREATMENT OF INTIMAL HYPERPLASIA  
JOURNAL Patent: WO 9820027-A 7 14-MAY-1998;  
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US-09-884-050-2 (1-141) x A92248 (1-696)

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Db 121 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCAATCGAGACCTCGTGGAC 180  
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

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Run on: November 20, 2002, 04:59:33 ; Search time 56 seconds

(without alignments)

953.589 Million cell updates/sec

Title: US-09-884-050-2

Perfect score: 792

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Searched: 335578 seqs, 189365133 residues

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Maximum Match 100%

Listing first 45 summaries

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#### SUMMARIES

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2	792	100.0	815	10	US-09-795-006A-146 Sequence 146, App
3	787	99.4	480	10	US-09-365-029-93 Sequence 93, Appli
4	787	99.4	576	10	US-09-932-451A-1 Sequence 1, Appli

5	787	99.4	649	10	US-09-349-954A-1	Sequence 1, Appli
6	787	99.4	649	10	US-09-907-007-1	Sequence 1, Appli
7	787	99.4	990	10	US-09-880-107-2336	Sequence 2336, Ap
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9	787	99.4	1736	12	US-10-044-090-164	Sequence 164, App
10	787	99.4	3583	9	US-09-981-353-185	Sequence 185, App
11	715	90.3	459	10	US-09-867-701-10298	Sequence 10298, A
12	663.5	83.8	2361	10	US-09-925-299-154	Sequence 154, App
13	583	73.6	388	10	US-09-795-006A-82	Sequence 82, Appl
14	521.5	65.8	391	10	US-09-795-006A-90	Sequence 90, Appl
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16	506	63.9	322	10	US-09-795-006A-50	Sequence 50, Appl
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33	413.5	52.2	391	10	US-09-795-006A-162	Sequence 162, App
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#### ALIGNMENTS

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; Sequence 1, Application US/09812133
; Patent No. US20020065240A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Kenneth A., Jr.
; APPLICANT: Kendall, Richard L.
; APPLICANT: Bett, Andrew J.
; APPLICANT: Huckle, William R.
; TITLE OF INVENTION: GENE THERAPY FOR STIMULATION OF ANGIOGENESIS
; FILE REFERENCE: 20073P
; CURRENT APPLICATION NUMBER: US/09/812,133
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/22668
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: 60/063,629
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Human
US-09-812-133-1
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; Patent No. US20020111324A1  
; GENERAL INFORMATION:  
; APPLICANT: OZAWA, Keiya  
; APPLICANT: SHIMPO, Masahisa  
; APPLICANT: IKEDA, Uichi  
; APPLICANT: MAEDA, Yoshikazu  
; APPLICANT: SHIMADA, Kazuyuki  
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-MEDIATED DELIVERY OF ANGIOGENIC  
; FILE REFERENCE: 0800-0026  
; CURRENT APPLICATION NUMBER: US/09/932,451A  
; CURRENT FILING DATE: 2001-08-17  
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US-09-932-451A-1

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; GENERAL INFORMATION:  
; APPLICANT: Hayward, Nicholas K.  
; APPLICANT: Weber, Gunther  
; APPLICANT: Grimmond, Sean  
; APPLICANT: No. US20020019027A1denskjold, Magnus  
; APPLICANT: Larsson, Catharina  
; TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING  
; FILE REFERENCE: Dav. COL. Cave  
; CURRENT APPLICATION NUMBER: US/09/349,954A  
; CURRENT FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: 08/765,588  
; PRIOR FILING DATE: 1996-02-22  
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US-09-349-954A-1

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; APPLICANT: Weber, Gunther  
; APPLICANT: Grimmond, Sean  
; APPLICANT: No. US20020142395Aldenskjoeld, Magnus  
; APPLICANT: Larsson, Catharina  
; TITLE OF INVENTION: A NOVEL GROWTH FACTOR AND A GENETIC SEQUENCE ENCODING  
; FILE REFERENCE: SAME  
; CURRENT APPLICATION NUMBER: US/09/907,007  
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; PRIOR APPLICATION NUMBER: 08/765,588  
; PRIOR FILING DATE: 1996-02-22  
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Db 77 GCCAAGTGTCCAGGCTCCACCATGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 136  
QY 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
Db 137 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCTTGGTGGAC 196  
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QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
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; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2336  
; LENGTH: 990  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M32977  
US-09-880-107-2336  
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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 99.37% Indels: 0  
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Db 117 GCCAAGTGTCCAGGCTCCACCATGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 176  
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Db 177 GTGAAGTTCATGGATGCTATCAGCGCAGCTACTGCCATCCCAATCGAGACCTTGGTGGAC 236  
QY 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
Db 237 ATCTTCCAGGAGTACCTGTATGAGATCGAGTACATCTTCAAGCCCATCTGTGTGCCCTG 296  
QY 81 MetArgCysGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
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QY 101 AsnileThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120  
Db 357 AACATCACCATGCGATGATGCGATCAACCTCACCAGGCCAGCACATAGGAGATG 416  
QY 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
Db 417 AGCTTCCTACAGCACAAACAAATGTGAATGCAGACCAAGAAAGATAGAGACAAGAA 476  
RESULT 8  
US-09-795-006A-1  
; Sequence 1, Application US/09795006A  
; Patent No. US20020151680A1

:	LENGTH:	1736
:	TYPE:	DNA
:	ORGANISM:	Homo sapiens
:	FEATURE:	
:	NAME/KEY:	misc_feature
:	OTHER INFORMATION:	IncYTE ID No. US20020137081A1 3348156CBI
:	NAME/KEY:	unsure
:	LOCATION:	1434, 1438-1439, 1512, 1514, 1521-1522, 1530
:	OTHER INFORMATION:	a, t, c, g, or other
:	US-10-044-090-164	
Alignment Scores:		
Pred. No.:	8.95e-96	Length: 1736
Score:	787.00	Matches: 140
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	99.37%	Indels: 0
DB:	12	Gaps: 0
US-09-884-050-2 (1-141) x US-10-044-090-164 (1-1736)		
Qy	1	MetAsnPheLeuSerTrpValHisTspSerLeuAlaLeuLeuTyThrLeuHisHis 20
Db	150	ATGAACFTTCGTGCTTGCGGGTCATTGGAGCCCTTGCCCTTGCTCTACCCTCCACCAT 209
Qy	21	AlaLysTrpSerGlnLaLaIaProMetAlaGluGlyGlyGlnAsnHisGluVal 40
Db	210	GCCAAAGTGGTCCCAGGCTGCCACCCATGGCAGAAGGAGGGGCAGAAATCATCACGAAGTG 269
Qy	41	VallysPheMetAspValTyRGinArgSerTyrCysHisProIleGluThrLeuValasp 60
Db	270	GTGAAGTTTCATGGATGCTATCAGCGCAGCTACTGCATCCAATCAGACCCCTGGTGGAC 329
Qy	61	IlePheGlnGluTyRProAspGluIleGluTyRIlePheLysProSerCysValProLeu 80
Db	330	ATCTTCAGAGTAGACCCGTGATGAGATCGAGTAGACATCTCAAGCCATCCTGTGTGCCCTG 389
Qy	81	MetArgCysGlyGlyCysCysAsnAspGluGlyLeuCysValProThrGluGluSer 100
Db	390	ATGCGATGCGGGGCTGCTCCATGACGAGGGCTGGAGTGTGTGCCACTGAGGAGTCC 449
Qy	101	AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120
Db	450	AACATCACCATGCAGATTATGCGGATCAAACCTCACCAAGGCCAGCACATAGGAGAGATG 509
Qy	121	SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspargAlaargGlnGlu 140
Db	510	AGCTTCTACAGCACACAATAATGTGAATGCAGACCAAGAAAGATAGACCAAGACAAGAA 569
RESULT 10		
US-09-981-353-185		
:	Sequence 185, Application	US/09981353
:	Patent No.	US20020160382A1
:	GENERAL INFORMATION:	
:	APPLICANT:	Lasek, Amy W.
:	APPLICANT:	Jones, David A.
:	TITLE OF INVENTION:	GENES EXPRESSED IN COLON CANCER
:	FILE REFERENCE:	PA-0038 US
:	CURRENT APPLICATION NUMBER:	US/09/981,353
:	CURRENT FILING DATE:	2001-10-11
:	NUMBER OF SEQ ID NOS:	194
:	SOFTWARE:	PERL Program
:	SEQ ID NO 185	
:	LENGTH:	3583
:	TYPE:	DNA
:	ORGANISM:	Homo sapiens
:	FEATURE:	
:	NAME/KEY:	misc_feature
:	OTHER INFORMATION:	IncYTE ID No. US20020160382A1 1384719.3
:	NAME/KEY:	unsure
:	LOCATION:	3245, 3265
:	OTHER INFORMATION:	a, t, c, g, or other
:	US-09-981-353-185	

US-09-884-050-2 (1-141) x US-09-867-701-10298 (1-459)

Qy	94	CysValproThrGluGluSerAsnIleThrMetGlnIleMetArgIleLysProHisGln	113
Db	188	TGGTGTCCCAACCAGAGAGTCCACATCACCATGCAGATTATGAGAATTAAACCTCACC	247
Qy	114	GlyGlnHisIleGlyGluMetSerPheLeuGlnHisAsnLysCysGluCysArgProLys	133
Db	248	GGCAGCACATCGGAGAGATGAGCTTTCTCCAGCATAAACAAATGTGAATGTAGACCA	307
Qy	134	LysAspArgAlaArgGlnGluLys	141
Db	308	AAAGATTGTGCTTCGAAACAAAAA	331

```

RESULT 14
US-09-795-006A-82
; Sequence 82, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hybrid DNA
; NAME/KEY: CDS
; LOCATION: (8)..(388)
US-09-795-006A-82

```

Alignment Scores:		
Pred. No.:	3,795-61	Length:
Score:	521.50	Matches:
Percent Similarity:	92.66%	Conservative:
Best Local Similarity:	86.24%	Mismatches:
Query Match:	65.85%	Indels:
DB:	10	Gaps:
US-09-884-050-2 (1-141)	x	US-09-795-006A-82 (1-391)

QY	34	GlyGlnAsnHisHisGlnValValLysPheMetAsp--ValTyrGlnArgSerTyrCys	52
DB	8	GGGCGAAGTATCATCCGAAGTGGTGAATCTATTGTAATAGTGGAGAAGACATCAGTCG	67
QY	53	HisProIleGluThrLeuValAspIlePheGlnGluTyrProAspGluIleGluTyrIle	72
DB	68	ATCGCATCGAGACACTGGTGGGACATCTTCCAGGAATACCTGATCAGATCGAGTACATC	127
QY	73	PheIysProSerCysValProLeuMetArgCysGlyCysCysAsnAspGluGlyLeu	92
DB	128	TTCAAGCCATCTCGTGGCCCCGTATGATGATGGGGGTTCGTGCAATGACGAAGGGCTG	187
QY	93	GluCysValProThrGluGluSerAsnIleThrMetGlnIleMetArgIleLysProHis	112
DB	188	GAGTGGCTTCCCAACCGAGGAGTCCAACATCACCATCGAGATTATGAGAATTAAACCTCAC	247
QY	113	GlnGlyClnHisIleGlyGluMetSerPheLeuGlnHisAsnLysCysGluCysArgPro	132
DB	248	CAAGGCGAGCAGCATCGGAGAGATGAGCTTTCTCCAGCATAAACAATGTGAATGTAGACCA	307
QY	133	LysLysAspArgAlaArgGlnGluLys	141
DB	308	AAGAAGATTTGGTCTTCGAAACAAAA	334

## RESULT 15

US-09-795-006A-86  
; Sequence 86, Application US/09795006A  
; Patent No. US20020151680A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo et al  
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR  
; FILE REFERENCE: 28967/35977B  
; CURRENT APPLICATION NUMBER: US/09/795,006A  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: US 60/205,331  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: US 60/185,205  
; PRIOR FILING DATE: 2000-02-25  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 86  
; LENGTH: 391  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Hybrid DNA  
; NAME/KEY: CDS  
; LOCATION: (8)..(388)  
US-09-795-006A-86

Alignment Scores:  
Pred. No.: 6 09e-60 Length: 391  
Score: 512.50 Matches: 92  
Percent Similarity: 91.74% Conservative: 8  
Best Local Similarity: 84.40% Mismatches: 8  
Query Match: 64.71% Indels: 1  
DB: 10 Gaps: 1

US-09-884-050-2 (1-141) x US-09-795-006A-86 (1-391)

QY	34	GlyGlnAsnHisGluValValLysPheMetAsp---ValTyrGlnArgSerTyrCys	52
DB	8	GGGCAGAAATCATCACCAAGTGGTGAATCTATTGATAATGAGTGGAGAAAGACTCAGTGC	67
QY	53	HisProIleGluThrLeuValAspIlePheGlnGluTyrProAspGluIleGluTyrIle	72
DB	68	ATGCCGATCGAGACACTGTGGACATCTCCAGGAATACCCCTGATGAGATCGAGTACATC	127
QY	73	PheLysProSerCysValProLeuMetArgCysGlyCysCysAsnAspGluGlyLeu	92
DB	128	TTCACCCATCTCTGCGTGCCTCGATGAGATGTGGGGTGTGCTGCAATAGTAGGGGCTG	187
QY	93	GluCysValProThrGluGluSerAsnIleThrMetGlnIleMetArgIleLysProHis	112
DB	188	CAGTGGTTCCTCCACCCAGGAGTCCACATCACCATGCAGATTATGAGATTAAACCTCAC	247
QY	113	GlnGlyGlnHisIleGlyGluMetSerPheLeuGlnHisAsnLysCysGluCysArgPro	132
DB	248	CAAGGGCAGACATCGAGAGATGAGCTTCTCCAGCATAACAAATGTGAATGTAGACCA	307
QY	133	LysLysAspArgAlaArgGlnGluLys	141
DB	308	AAGAAGATTGTGCTTCGACAAAAA	334

Search completed: November 20, 2002, 05:08:46  
Job time : 62 secs



GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 20, 2002, 05:01:43 ; Search time 2138 Seconds  
(without alignments)  
1068.084 Million cell updates/sec

Title: US-09-884-050-2

Perfect score: 792

Sequence: 1 MNFLSWVHWSLALLYLHH.....FLQHNKCECRPKKDRARQEK 141

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -DOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FPGAPOP=6 -FPGAEXT=7  
-YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_Other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	749	94.6	528	14	BQ674897	BQ674897 AGENCOURT
2	715	90.3	459	9	AL591060	AL591060 tw28f02.x
3	681.5	86.0	752	14	BQ780197	BQ780197 UI-R-Ff0-
4	584.5	73.8	600	12	BG803325	BG803325 0223-76 M
5	552	69.7	890	13	BI869727	BI869727 603393614
6	503.5	63.6	719	12	BG864739	BG864739 603799154
7	390.5	49.3	600	12	BG802357	BG802357 0174-04 M
8	385	48.6	534	14	BM991154	BM991154 UI-H-D10-
9	382	48.2	649	12	BF679862	BF679862 602154448
10	353	44.6	208	10	BE166230	BE166230 MR3-HT048
11	325	41.0	869	9	AL552344	AL552344 AL552344
12	325	41.0	890	14	BQ644755	BQ644755 AGENCOURT
13	325	41.0	901	9	AL552106	AL552106 AL552106
14	325	41.0	903	9	AL546005	AL546005 AL546005
15	325	41.0	925	9	AL547463	AL547463 AL547463
16	325	41.0	963	9	AL540600	AL540600 AL540600
17	325	41.0	963	14	BQ893335	BQ893335 AGENCOURT
18	325	41.0	1023	9	AL543185	AL543185 AL543185
19	325	41.0	1031	14	BQ070531	BQ070531 AGENCOURT
20	323	40.8	1073	14	BQ070196	BQ070196 AGENCOURT
21	318.5	40.2	489	13	BI790853	BI790853 id09h10.Y
22	318	40.2	792	9	AL545800	AL545800 AL545800
23	317	40.0	997	9	AL530856	AL530856 AL530856
24	316	39.9	900	14	BQ647895	BQ647895 AGENCOURT
25	314	39.6	829	10	BE569697	BE569697 601331496
26	314	39.6	887	14	BQ881520	BQ881520 AGENCOURT
27	314	39.6	933	14	BQ936933	BQ936933 AGENCOURT
28	314	39.6	936	13	BI905649	BI905649 603167660
29	313	39.5	744	13	BI663772	BI663772 603288511
30	312	39.4	455	9	AI272466	AI272466 uk06c06.Y
31	312	39.4	885	9	AL543693	AL543693 AL543693
32	304.5	38.4	621	13	BM487268	BM487268 pgmzn.pk0
33	304	38.4	786	9	AL551439	AL551439 AL551439
34	302.5	38.2	806	13	BI648112	BI648112 603278429
35	300	37.9	759	13	BI685632	BI685632 603309146
36	300	37.9	953	14	BQ713895	BQ713895 AGENCOURT
37	299	37.8	794	13	BI852987	BI852987 603379807
38	299	37.8	913	9	AL553367	AL553367 AL553367
39	294	37.1	724	13	BI692908	BI692908 603344629
40	293	37.0	364	9	AL838330	AL838330 AL838330
41	292	36.9	950	9	AL551942	AL551942 AL551942
42	291	36.7	733	13	BG923923	BG923923 602824355
43	290.5	36.7	874	10	BE570632	BE570632 601329939
44	290	36.6	347	12	BG003056	BG003056 MR3-GN018
45	289.5	36.6	957	12	BE791106	BE791106 601586286

#### ALIGNMENTS

RESULT 1  
BQ674897  
LOCUS BQ674897 528 bp mRNA linear EST 15-JUL-2002  
DEFINITION AGENCOURT\_8036450 NIH\_MGC\_102 Homo sapiens CDNA clone IMAGE:6212223  
5' mRNA sequence.  
ACCESSION BQ674897  
VERSION BQ674897.1 GI:21785731  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 528)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)



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Db 182 ATGCGATCGGGGCTGCTGAATACGAGGCGCTGGAGTGTGTGCCACTGAGGAGT 123
Qy 100 eRAsnileThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluM 120
Db 122 CCAACATCCCATGAGATTATGCGATCAACCTCACCAGGCCGACACATAGAGAGA 63
Qy 120 etSerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnG 140
Db 62 TGAGCTTCTACAGCCCAACAAATGTGAATGCAGACCAAAAAAAAAAAAAAAAAAAAA 3
Qy 140 lu 140
Db 2 AA 1

RESULT 3
BQ780197/c
LOCUS BQ780197 752 bp mRNA linear EST 26-JUL-2002
DEFINITION UI-R-FF0-cpb-i-06-0-UI.s1 UI-R-FF0 Rattus norvegicus cDNA clone
ACCESSION BQ780197
VERSION BQ780197.1 GI:21988669
KEYWORDS EST
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 752)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Jeff Stevens
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: DISTRIBUTION: Researchers may obtain clones
from Research Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-39, >POLY_A#Simple_repeat (matched complement) 546-578,
>GC-rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA-Yes.

FEATURES
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            /organism="Rattus norvegicus"
            /db_xref="taxon:10116"
            /clone="UI-R-FF0-cpb-i-06-0-UI"
            /clone_lib="UI-R-FF0"
            /tissue_type="Mixed tissues"
            /dev_stage="Adult"
            /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
            /note="Vector: pT7T3-Pac (Pharmacia) with a modified
polylinker; Site.1: EcoR I; Site.2: Not I; UI-R-FF0 is a
subtracted cDNA library containing the following tissue(s)
): Normal cartilage and SR-JWS Tumor Line . The
subtraction was made according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for these libraries are: CTAATGGAGC,
CAATCTTGTA.
TAG_LIB=UI-R-FF0

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TAG_TISSUE=cartilage
TAG_SEQ=CTAATGGAGC"
BASE COUNT 109 a 246 c 205 g 189 t 3 others
ORIGIN
Alignment Scores:
Pred. No.: 4.6e-74 Length: 752
Score: 681.50 Matches: 122
Percent Similarity: 90.78% Conservative: 6
Best Local Similarity: 86.52% Mismatches: 12
Query Match: 86.05% Indels: 1
DB: 14 Gaps: 1

US-09-884-050-2 (1-141) x B0780197 (1-752)
Qy 1 MetAsnPheLeuSerTyrValHisTyrPheLeuAlaLeuLeuTyrLeuHisHis 20
Db 431 ATGAATCTTCTGCTCTCTTGGTGCTGCTGGAGCCCTGGCTTTTACTGCTGTACCTCCACCAT 372
Qy 21 AlaLysTyrSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisHisGluVal 40
Db 371 GCCAAGTGTCCCGCTGCACCCACGACAGAA---GGGGACGACAGAAAGCCCATGAAGTG 315
Qy 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValasp 60
Db 314 GTGAAGTTTCATGGAGCTCTACCAGCGCAGCTATTGCCGTCCAATTGAGACCTGCTGGAC 255
Qy 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80
Db 254 ATCTTCCAGGATACCCCGATGATAGATAGATATATCTTCAAGCCGCTGTGTGCCCTTA 195
Qy 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100
Db 194 ATGCGGTGTGGGGTGTGCTGCAATGATGAAGCCCTGGAGTGGTCCCGACGTCGGAGAC 135
Qy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMet 120
Db 134 AACGTCACTATGCAGATCATGCGGATCAAACTCACCAGGCGCAGCACATAGAGAGATG 75
Qy 121 SerPheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140
Db 74 AGCTTCTGCGACGATAGCAGATGTGAATGCAGACCAAGAAAGATAGAACAAAGCCAAA 15
Qy 141 Lys 141
Db 14 AAA 12

RESULT 4
BQ803325
LOCUS BQ803325 600 bp mRNA linear EST 20-DEC-2001
DEFINITION 0223-76 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
mRNA sequence.
ACCESSION BQ803325
VERSION BQ803325.1 GI:17950226
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
Mu.X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,
White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.
Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
Nucleic Acids Res. 29 (24), 4983-4993 (2001)
21671825
Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
Location/Qualifiers
FEATURES

```

```

source
1..600
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/notes="Vector: pAMP10 (Gibco); Cloned unidirectionally.
Primer: Oligo dt. RNA isolation: cytoplasmic RNA preps
(Manniat); Cloning technique: CUA Cloning (Clontech,
Life Technologies); Average insert size: 1.8 Kb;
Insertion site: TAGTCCACCTGAATCTGAGTG-->. Other
information regarding entire library may be found at
http://pga.smed.edu/data/libraries/microarray_cdna_library
ies.htm."
BASE COUNT 131 a 183 c 196 g 90 t
ORIGIN

Alignment Scores:
Pred. No.: 3,71e-62 Length: 600
Score: 584.50 Matches: 106
Percent Similarity: 90.76% Conservative: 2
Best Local Similarity: 89.08% Mismatches: 10
Query Match: 73.80% Indels: 1
DB: 12 Gaps: 1

US-09-884-050-2 (1-141) x BG803325 (1-600)

Qy 1 MetAsnPheLeuSerTrpValHisTrpSerLeuAlaLeuLeuLeuHisHis 20
|||||
Db 246 ATGAACCTTCTGCTCTCTGGTGCACCTGGACCCCTGCTTACTGCTGACCTCCACCAT 305
|||||

Qy 21 AlaLysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluVal 40
|||||
Db 306 GCCAAGTGGTCCCGAGGTGCACCCACACAGAA---GGAGAGCAGAGTCCCATGAAGTG 362
|||||

Qy 41 ValLysPheMetAspValTrpGlnArgSerTrpCysHisProIleGluThrLeuValAsp 60
|||||
Db 363 ATCAAGTTCATGGATGCTACCGAGGAGTACTGCGCTCCGATGAGACCCCTGGTGGAC 422
|||||

Qy 61 IlePheGlnGluTrpProAspGluIleGluTrpIlePheLysProSerCysValProLeu 80
|||||
Db 423 ATCTTCAGGAGTACCCCGACGAGATAGATACATCTTCAAGCCGCTCTGTGCGCGCTG 482
|||||

Qy 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100
|||||
Db 483 ATGCGCTGTCGAGGCTGCTACAGATGAGCCCTGGAGTGGTCCCGCAGAGAGC 542
|||||

Qy 101 AsnIleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGlu 119
|||||
Db 543 AACATCACCATGCAGATCATGCGGATCAACACCTCACCAAGCCAGCACATAGAGAG 599
|||||

RESULT 5
BI869727 890 bp mRNA linear EST 11-OCT-2001
LOCUS 603393614F1 NTH_MGC_90 Homo sapiens cDNA clone IMAGE:5403771 5',
DEFINITION mRNA sequence.
ACCESSION BI869727
VERSION BI869727.1 GI:16043400
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 890)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM12029 row: k column: 04

High quality sequence stop: 733.

#### FEATURES

Location/Qualifiers  
 source 1..890  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:5403771"  
 /clone\_lib="NIH\_MGC\_90"  
 /tissue\_type="adenocarcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /notes="Organ: liver; Vector: PCMV-SPORT6; Site\_1: NotI;  
 Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 1.7 Kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

BASE COUNT 246 a 246 c 256 g 142 t  
 ORIGIN

#### Alignment Scores:

Pred. No.: 7.46e-58 Length: 890  
 Score: 552.00 Matches: 98  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 69.70% Indels: 0  
 DB: 13 Gaps: 0

US-09-884-050-2 (1-141) x BI869727 (1-890)

Qy 43 PheMetAspValTrpGlnArgSerTrpCysHisProIleGluThrLeuValAspIlePhe 62  
 |||||  
 Db 1 TTCATGGATGTCTATCAGCGCAGCTACTCCATCCATCCAGACCCCTGGTGGACATCTTC 60  
 |||||  
 Qy 63 GlnGluTrpProAspGluIleGluTrpIlePheLysProSerCysValProLeuMetArg 82  
 |||||  
 Db 61 CAGGAGTACCCCTGATGAGATCGAGTACATCTTCAAGCCATCCTGTGTCCTGATGCCA 120  
 |||||  
 Qy 83 CysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluSerAsnIle 102  
 |||||  
 Db 121 TCGGGGGCTGCTGCANTACGAGGCGCTGGAGTGTGCCCATGAGAGTCCCAATC 180  
 |||||  
 Qy 103 ThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMetSerPhe 122  
 |||||  
 Db 181 ACCATGCAGATTATCGGATCAACCTCACCAAGCCAGCACATAGAGAGATGAGCTTC 240  
 |||||  
 Qy 123 LeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGlu 140  
 |||||  
 Db 241 CTACAGCACACAAATGTGATGCAGACCAAGAAAGATAGAGCAAGCAAGAA 294  
 |||||

#### RESULT 6

BI864739 719 bp mRNA linear EST 29-MAY-2001  
 LOCUS 602799154F1 NCI\_CGAP\_Mam4 Mus musculus cDNA clone IMAGE:4934916 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI864739  
 VERSION BI864739.1 GI:14215277  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 REFERENCE 1 (bases 1 to 719)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth  
 Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM10864 row: k column: 13  
 High quality sequence stop: 715.  
 Location/Qualifiers  
 1. 719

#### FEATURES

source  
 1. 719  
 /organism="Mus musculus"  
 /strain="NMRI"  
 /db\_xref="taxon:10090"  
 /clone\_lib="NCI\_CGAP\_Mam4"  
 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="5 months"  
 /lab\_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Library constructed by Life Technologies. Investigators  
 providing samples: Lothar Hennighausen/Priscilla Furth,  
 NIH Reference for transgenic model: Li et al., Cell Growth  
 and Differentiation 7, 3-11 (1996)."

BASE COUNT 156 a 205 c 245 g 113 t

#### ORIGIN

Alignment Scores:  
 Pred. No.: 5.74e-52 Length: 719  
 Score: 503.50 Matches: 91  
 Percent Similarity: 90.29% Conservative: 2  
 Best Local Similarity: 88.35% Mismatches: 9  
 Query Match: 63.57% Indels: 1  
 DB: 12 Gaps: 1

US-09-884-050-2 (1-141) x BG864739 (1-719)

Qy 1 MetAsnPheLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20  
 Db 312 ATGAACCTTCGCTCTCTGGTGCACTGGACCCCTGGCTTACTGCTACCTCCACCAT 371  
 Qy 21 AlaLysTrpSerGlnAlaAlaProMetaLgLuGlyGlyGlnAsnHisGluVal 40  
 Db 372 GCCAAGTGTCCAGCTGCACCCACGACAGAA---GGAGAGCAGAAATCCCATGAAGTG 428  
 Qy 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
 Db 429 ATCAAGTTCATGGATGTCTACCAGGAGAGCTACTCCGCTCCGATTCGAGACCCCTGGTGAC 488  
 Qy 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
 Db 489 ATCTTCCAGGAGTACCCCGACGAGATAGATACATCTTCAAGCCGCTCCTGTGTGCGCGTG 548  
 Qy 81 MetArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSer 100  
 Db 549 ATGCGCTGTGAGGCTGTGTAAACATGAAGCCCTGGAGTGGTCCCGCCACGTCAGAGAGC 608  
 Qy 101 AsnIleThr 103  
 Db 609 AACATCACC 617

#### RESULT 7

BG802357 600 bp mRNA linear EST 20-DEC-2001  
 LOCUS 0174-04 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,  
 DEFINITION mRNA sequence.  
 ACCESSION BG802357  
 VERSION BG802357.1 GI:17949245  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 600)  
 REFERENCE Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,  
 AUTHORS

White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.  
 Gene expression in the developing mouse retina by EST sequencing  
 and microarray analysis  
 Nucleic Acids res. 29 (24), 4983-4993 (2001)

#### JOURNAL

#### MEDLINE

COMMENT  
 Contact: Klein WH  
 Department of Biochemistry and Molecular Biology  
 University of Texas M.D. Anderson Cancer Center  
 Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA  
 Tel: 713 792 3646  
 Fax: 713 790 0329.

#### FEATURES

##### Location/Qualifiers

1. 600  
 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /clone\_lib="Mouse E14.5 retina lambda ZAP II Library"  
 /tissue\_type="neural retina"  
 /dev\_stage="embryonic day 14.5 post-fertilization"  
 /note="vector: pAMP10 (Gibco); Cloned unidirectionally.  
 Primer: Oligo dt. RNA isolation: cytoplasmic RNA preps  
 (Mannatis); Cloning Technique: CUA Cloning (CloneAmp,  
 Life Technologies); Average insert size: 1.8 Kb;  
 Insertion site: TAGTCCACTGAATTCGAGTG--->. Other  
 information regarding entire library may be found at  
[http://pga.swmed.edu/Data/Libraries/microarray\\_cdna\\_libraries.htm](http://pga.swmed.edu/Data/Libraries/microarray_cdna_libraries.htm).

BASE COUNT 121 a 180 c 210 g 89 t

#### ORIGIN

Alignment Scores:  
 Pred. No.: 4.83e-38 Length: 600  
 Score: 390.50 Matches: 72  
 Percent Similarity: 91.36% Conservative: 2  
 Best Local Similarity: 88.89% Mismatches: 6  
 Query Match: 49.31% Indels: 1  
 DB: 12 Gaps: 1

US-09-884-050-2 (1-141) x BG802357 (1-600)

Qy 1 MetAsnPheLeuSerTrpValHisTrpSerLeuAlaLeuLeuTyrLeuHisHis 20  
 Db 359 ATGAACCTTCGCTCTCTGGTGCACTGGACCCCTGGCTTACTGCTACCTCCACCAT 418  
 Qy 21 AlaLysTrpSerGlnAlaAlaProMetaLgLuGlyGlyGlnAsnHisGluVal 40  
 Db 419 GCCAAGTGTCCAGCTGCACCCACGACAGAA---GGAGAGCAGAAATCCCATGAAGTG 475  
 Qy 41 ValLysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAsp 60  
 Db 476 ATCAAGTTCATGGATGTCTACCAGGAGAGCTACTCCGCTCCGATTCGAGACCCCTGGTGAC 535  
 Qy 61 IlePheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeu 80  
 Db 536 ATCTTCCAGGAGTACCCCGACGAGATAGATACATCTTCAAGCCGCTCCTGTGTGCGCGTG 595  
 Qy 81 Met 81  
 Db 596 ATG 598

#### RESULT 8

BW991154/c 534 bp mRNA linear EST 17-JUN-2002  
 LOCUS UI-H-DIO-atp-h-22-0-UI.s1 NCI\_CGAP\_DIO Homo sapiens cDNA clone  
 DEFINITION IMAGE:5862597 3', mRNA sequence.  
 ACCESSION BW991154  
 VERSION BW991154.1 GI:19710543  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 534)  
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS

**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-re@mail.nih.gov  
 Tissue Procurement: Dr. Jose Mercuende  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Seq primer: M3 FORWARD  
 POLIA=yes

# FEATURES

## Location/Qualifiers

1. .534  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5862597"  
 /clone\_lib="NCI\_CGAP\_DI0"  
 /tissue\_type="Lung Focal Fibrosis"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI\_CGAP\_DI0 is a cDNA library containing the following tissue(s): A pool of Lung Focal Fibrosis. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ATAGCGGTCG."

TAG\_LIB=UI-H-DI0  
 TAG\_TISSUE=lung with fibrosis  
 TAG\_SEQ=ATAGCGGTCG"

**BASE COUNT** 88 a 145 c 136 g 165 t

## ORIGIN

**Alignment Scores:**  
 Pred. No.: 1.95e-37 Length: 534  
 Score: 385.00 Matches: 68  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 48.61% Indels: 0  
 DB: 14 Gaps: 0

US-09-884-050-2 (1-141) x BM991154 (1-534)

QY 74 LysProSerCysValProLeuMetArgCysGlyGlyCysAsnAspGluGlyLeuGlu 93  
 DB 525 AAGCCATCTGTGTGCCCTGATGCGATCGGGGGCTGCTGCAATGACGAGGCGCTGGAG 466  
 QY 94 CysValProThrGluGluSerAsnIleThrMetGlnIleMetArgIleLysProHisGln 113  
 DB 465 TGTGTGCCCACTGAGGAGTCCACATCACCATGCAGATTATGCGGATCAACCTCACAA 406  
 QY 114 GlyGlnHisIleGlyGluMetSerPheLeuGlnHisAsnLysCysGluCysArgProLys 133  
 DB 405 GCCCAGCACATAGGAGATGAGCTTCCTACAGCACAAACAAATGTGATGCAGACCAAG 346  
 QY 134 LysAspArgAlaArgGingLulys 141  
 DB 345 AAAGATAGACGACAGACAGAAAAA 322

## RESULT 9

BF679862  
 LOCUS BE166230 649 bp mRNA linear EST 21-DEC-2000  
 DEFINITION 602154448F1 NIH\_MGC\_83 Homo sapiens cDNA clone IMAGE:4295651 5', mRNA sequence.

# ACCESSION

BF679862.1 GI:11953671

## KEYWORDS

EST.

## SOURCE

human.

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 649)

## AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

## TITLE

Unpublished (1999)

## JOURNAL

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-re@mail.nih.gov  
 Tissue Procurement: CLONETECH Laboratories, Inc.  
 cDNA Library Preparation: CLONETECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLCML146 row: 0 column: 12

High quality sequence stop: 524.

## FEATURES

### source

1. .649  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4295651"  
 /clone\_lib="NIH\_MGC\_83"  
 /lab\_host="DH10B (TI phage-resistant)"  
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site\_1: SfiI (ggccgctcgcc); Site\_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

**BASE COUNT** 197 a 140 c 181 g 131 t

## ORIGIN

**Alignment Scores:**  
 Pred. No.: 6.21e-37 Length: 649  
 Score: 382.00 Matches: 70  
 Percent Similarity: 95.95% Conservative: 1  
 Best Local Similarity: 94.59% Mismatches: 2  
 Query Match: 48.23% Indels: 1  
 DB: 12 Gaps: 0

US-09-884-050-2 (1-141) x BF679862 (1-649)

QY 47 TyrGlnArgSerTyrCysHisProIleGluThrLeuValAspIlePheGlnGluTyrPro 66  
 DB 3 TATCAGCGAGCTACTGCATCAATCGAGACCTCGTGACATCTTCAGGAGTAGTACCCT 62  
 QY 67 AspGluIleGluTyrIlePheLysProSerCysValProLeuMetArgCysGlyGlyCys 86  
 DB 63 GATGAGATCGAGTACATCTTCAAGCCATCCTGTGTGCCCTGATGCGATGCGGGGCTGC 122  
 QY 87 CysAsnAspGluGlyLeuGluCysValProThrGluGluSerAsnIleThrMetGlnIle 106  
 DB 123 TCGAATGACGAGGGCGCTGGAGTGTGTGCCACTGAGGAGTCCCAACATCACCATGCAGATT 182  
 QY 107 MetArgIleLysProHisGlnGlyGln-HisIleGlyGlu 119  
 DB 183 ATGCGGATCAAACTCAAGAGGCCAACACATTCGCGAA 222

## RESULT 10

BE166230  
 LOCUS BE166230 208 bp mRNA linear EST 21-JUN-2000  
 DEFINITION MR3-HT0489-010300-104-g01 HT0489 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BE166230

VERSION BE166230.1 GI:8628951  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 208)  
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and  
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT 20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-MR3-HT0489-010>)

300-104-g01a3-2000-03-01&t4=1

Seq primer: puc 18 forward

High quality sequence stop: 208.

Location/Qualifiers

FEATURES

source

1..208

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="HT0489"

/dev\_stage="Adult"

/note="Organ: head\_neck; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

BASE COUNT 51 a 57 c 56 g 44 t

ORIGIN

Alignment Scores:

Pred. No.: 4.34e-34 Length: 208

Score: 353.00 Matches: 67

Percent Similarity: 97.10% Conservative: 0

Best Local Similarity: 97.10% Mismatches: 2

Query Match: 44.57% Indels: 1

DB: 10 Gaps: 0

US-09-884-050-2 (1-141) x BE166230 (1-208)

QY 54 ProfileGluThrLeuValAspIlePheGlnGluTyrProAspGluIleGluTyrIlePhe 73

Db 2 CCAATCGAGACCTTGATGAC-ATCTTCAGGAGTACCCTGATGAGATCGAGTACATCTTC 60

QY 74 LysProSerCysValProLeuMetArgCysGlyGlyCysAsnAspGluGlyLeuGlu 93

Db 61 AAGCCATCTGTGTCCTGATGCGATGCGGGGCTGCTGCAATGACGAGGCTCGAG 120

QY 94 CysValProThrGluGluSerAsnIleThrMetGlnIleMetArgIleLysProHisGln 113

Db 121 TGTGTGCCACTGAGGAGTCCAAATCACCATGACAGATTATCGGATCAAACTCACCA 180

QY 114 GlyGlnHisIleGlyGluMetSerPhe 122

Db 181 GGCCAGCACATAGGAGATGAGCTTC 207

RESULT 11

AL552344

DEFINITION

prime, mRNA sequence.

ACCESSION

AL552344

VERSION

AL552344.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 869)

AUTHORS

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished (2001)

COMMENT

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr).

FEATURES

Location/Qualifiers

1..869

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="CS0D1069YH16"

/clone\_lib="LTI\_NFL006\_PL2"

/tissue\_type="placenta"

/note="Vector: pCMVSPORT 6; Site\_1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-stranded cDNA was digested with Not I and

cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact : Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :

<http://fulllength.invitrogen.com>"

BASE COUNT 141 a 287 c 293 g 144 t

ORIGIN

Alignment Scores:

Pred. No.: 1.18e-29 Length: 869

Score: 325.00 Matches: 55

Percent Similarity: 67.50% Conservative: 26

Best Local Similarity: 45.83% Mismatches: 35

Query Match: 41.04% Indels: 4

DB: 9 Gaps: 1

US-09-884-050-2 (1-141) x AL552344 (1-869)

QY 22 LysTrpSerGlnAlaAlaProMetAlaGluGlyGlyGlnAsnHisGluValVal 41

Db 414 CAGTGGCGCTTCTCTGCT-----GGGACGGCTCTCAGAGGTGGAATGGTA 461

QY 42 LysPheMetAspValTyrGlnArgSertyrCysHisProIleGluThrLeuValAspIle 61

Db 462 CCCTTCCAGGAAGTGTGGGGCGCAGCTACTGCCGGCGCTGAGAGGCTGTGGAGCTC 521

QY 62 PheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeuMet 81

Db 522 GTGTCCGAGTACCCAGGAGGTGGAGCACATGTTTCAGCCCATCTGTCTCTCCCTG 581

QY 82 ArgCysGlyGlyCysCysAsnAspGluGlyLeuGlyCysValProThrGluGluSerAsn 101

Db 582 CCCTACACGGCTGCTGGCGGATGAGAACTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 641

QY 102 IleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMetSer 121

Db 642 GTCACCATGACAGCTCTTAAGATCCGTTCTGGGGACCGCCCTCTACGTGGAGCTG 701

QY 122 PheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGluLys 141

Db 702 TTCTCTACGACGTTTCGCTGCGAATGCGGGCTCTGCGGGAGAGATGAAGCGCGAAGG 761

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RESULT 12
BQ644755      890 bp      mRNA      linear      EST 15-JUL-2002
LOCUS          AGENCOURT_8540206 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6297259
DEFINITION    5', mRNA sequence.
ACCESSION     BQ644755
VERSION       BQ644755.1 GI:21768927
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 890)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: CGAP (Stanford)
              cDNA Library Preparation: Rubin Laboratory
              DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLCM2506 row: g column: 20
              High quality sequence stop: 662.
FEATURES     source
             1..890
             Location/Qualifiers
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:6297259"
               /clone_lib="NIH_MGC_100"
               /tissue_type="hepatocellular carcinoma, cell line"
               /lab_host="DH10B (phage-resistant)"
               /note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
               EcoRI; cDNA made by oligo-dT priming. Directionally cloned
               into EcoRI/XhoI sites using the following 5' adaptor:
               GGCAGGAG(G). Size-selected >500bp for average insert size
               1.8kb. Library constructed by Ling Hong in the laboratory
               of Gerald M. Rubin (University of California, Berkeley)
               using ZAP-cDNA synthesis kit (Stratagene) and Superscript
               II RT (Life Technologies). Note: this is a NIH_MGC
               Library."
BASE COUNT   183 a 259 c 265 g 182 t 1 others
ORIGIN
Alignment Scores:
Pred. No.:   1.23e-29      Length:      890
Score:       325.00      Matches:      55
Percent Similarity: 67.50%      Conservative: 26
Best Local Similarity: 45.83%      Mismatches:  35
Query Match: 41.04%      Indels:      4
DB:          14          Gaps:         1

US-09-884-050-2 (1-141) x BQ644755 (1-890)

QY  22 LysTrpSerGlnAlaProMetAlaGluGlyGlyGlnAsnHisGluValVal 41
Db  290 CAGTGGCGCTGTCGTCT-----GGGAACGGCTCGTCAGAGGTGGAAGTGTA 337
QY  42 LysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAspIle 61
Db  338 CCTTCCAGAGAGTGGGGCGGCAGCTACTCGGGCGCTCGAGAGGTGTGTGACGTC 397
QY  62 PheGlnGluTyrProAspGluLeuGlyTyrIlePheLysProSerCysValProLeuMet 81
Db  398 GTGTCCGAGTACCCAGCGAGGTGGAGCACATGTTTCAGCCCATCTGTCTCTCCCTGTG 457
QY  82 ArgCysGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluSerAsn 101
Db  458 CGCTGCACCGCGCTGTGGCGGCATGAGAACTCTGCCTGTGTCGGGTGGAGACGCCCAAT 517

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QY  102 IleThrMetGlnIleMetArgTyleLysProHisGlnGlyGlnHisIleGlyGluMetSer 121
Db  518 GTCACCATGACGCTCTTAAGATCGCTTGGGGACCGCCCTCTACCTGAGCTGAGC 577
QY  122 PheLeuGlnHisAsnLysCysGluCysArgProLysLysAspAlaArgGlnGluLys 141
Db  578 TTCTCTCAGCAGCTTCGCTGCGAATGCGCGCTCTGCGGGAGAAGATGAAGCGGAAGG 637

RESULT 13
AL552106      901 bp      mRNA      linear      EST 16-FEB-2001
LOCUS          AL552106 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI059N23 5
DEFINITION    prime, mRNA sequence.
ACCESSION     AL552106
VERSION       AL552106.1 GI:12890686
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 901)
AUTHORS      Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE        Full-length cDNA libraries and normalization
JOURNAL      Unpublished (2001)
COMMENT      Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 EVRY cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES     source
             1..901
             Location/Qualifiers
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="CSODI059N23"
               /clone_lib="LTI_NFL006_PL2"
               /tissue_type="placenta"
               /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
               was primed with a NotI-oligo(dT) primer. Five prime end
               enriched, double-stranded cDNA was digested with Not I and
               cloned into the Not I and Eco RV sites of the pCMVSPORT 6
               vector. Library was normalized. Library was constructed by
               Life Technologies. Contact : Feng Liang Life Technologies,
               a division of Invitrogen 9800 Medical Center Drive
               Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
               Email : fliang@lifetech.com URL :
               http://fulllength.invitrogen.com"
BASE COUNT   148 a 298 c 299 g 153 t 3 others
ORIGIN
Alignment Scores:
Pred. No.:   1.25e-29      Length:      901
Score:       325.00      Matches:      55
Percent Similarity: 67.50%      Conservative: 26
Best Local Similarity: 45.83%      Mismatches:  35
Query Match: 41.04%      Indels:      4
DB:          9          Gaps:         1

US-09-884-050-2 (1-141) x AL552106 (1-901)

QY  22 LysTrpSerGlnAlaProMetAlaGluGlyGlyGlnAsnHisGluValVal 41
Db  407 CAGTGGCGCTGTCGTCT-----GGGAACGGCTCGTCAGAGGTGGAAGTGTA 454
QY  42 LysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAspIle 61
Db  455 CCTTCCAGAGAGTGGGGCGGCAGCTACTCGGGCGCTGGAGAGGTGTGTGACGTC 514
QY  62 PheGlnGluTyrProAspGluLeuGlyTyrIlePheLysProSerCysValProLeuMet 81
Db  515 GTGTCCGAGTACCCAGCGAGGTGGAGCACATGTTTCAGCCCATCTGTCTCTCCCTGTG 574
QY  82 ArgCysGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluSerAsn 101
Db  458 CGCTGCACCGCGCTGTGGCGGCATGAGAACTCTGCCTGTGTCGGGTGGAGACGCCCAAT 517

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Db 575 CGTGCACCGGCTGCTGGCGGATGAGAAATCTGCACCTGTGTGCGGTGGAGACGCCCAAT 634
Qy 102 IletHrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMetSer 121
   ::::::::::::::::::::::::::::
Db 635 GTCACCATGACGCTCTAAAGATCCGTCTGCGGACCGCCCTCTAGCTGAGCTGACG 694
   ::::::::::::::::::::::::::::
Qy 122 PheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaAraGlnGluLys 141
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Db 695 TTCTCTCAGCAGCTTGCCTGCGAATGCGCGCTCTGCGGAGAGATGAAGCCGGAAGG 754

RESULT 14
AL546005
LOCUS
DEFINITION AL546005 LTI_NFL006_PL2 903 bp mRNA linear EST 16-FEB-2001
prime, mRNA sequence.
ACCESSION AL546005
VERSION AL546005.1 GI:12878718
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 903)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/db_xref="taxon:9606"
/clone="CS0D1024YG09"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/notes="Vector: pCMVSPORT 6; Site:1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 148 a 296 c 294 g 157 t 8 others
ORIGIN
Alignment Scores:
Pred. No.: 1.26e-29 Length: 903
Score: 325.00 Matches: 55
Percent Similarity: 67.50% Conservative: 26
Best Local Similarity: 45.83% Mismatches: 35
Query Match: 41.04% Indels: 4
DB: 9 Gaps: 1

US-09-884-050-2 (1-141) x AL546005 (1-903)
Qy 22 LysTrpSerGlnAlaProMetAlaGluGlyGlyGlnAsnHisHisGluValVal 41
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Db 400 CAGTGGGCTTGTCTGCT-----GGGAACGCTCTGTCAGAGGTGAAGTGTA 447
   ::::::::::::::::::::
Qy 42 LysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAspIle 61
   ||| ::::::::::::::::::::
Db 448 CCCTTCCAGGAAGTGTGGGCGGACGACTACTGCCGGCGCTGGAGAGGCTGGTGCACGTC 507
   ||| ::::::::::::::::::::
Qy 62 PheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeuMet 81
   ||||| ::::::::::::::::::::
Db 508 GTGTCCGAGTACCCAGGAGGTGGAGCAATGTTACACCCATCTGTGTCTCCCTGCTG 567
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Qy 82 ArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluLysAsn 101

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Db 568 CGTGCACCGGCTGCTGGCGGATGAGAAATCTGCACCTGTGTGCGGTGGAGACGCCCAAT 627
Qy 102 IletHrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMetSer 121
   ::::::::::::::::::::::::::::
Db 628 GTCACCATGACGCTCTAAAGATCCGTCTGCGGACCGCCCTCTAGCTGAGCTGACG 687
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Qy 122 PheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaAraGlnGluLys 141
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Db 688 TTCTCTCAGCAGCTTGCCTGCGAATGCGCGCTCTGCGGAGAGATGAAGCCGGAAGG 747

RESULT 15
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LOCUS
DEFINITION AL547463 LTI_NFL006_PL2 925 bp mRNA linear EST 16-FEB-2001
prime, mRNA sequence.
ACCESSION AL547463
VERSION AL547463.1 GI:12881556
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 925)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/tissue_type="placenta"
/notes="Vector: pCMVSPORT 6; Site:1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 148 a 309 c 301 g 161 t 6 others
ORIGIN
Alignment Scores:
Pred. No.: 1.3e-29 Length: 925
Score: 325.00 Matches: 55
Percent Similarity: 67.50% Conservative: 26
Best Local Similarity: 45.83% Mismatches: 35
Query Match: 41.04% Indels: 4
DB: 9 Gaps: 1

US-09-884-050-2 (1-141) x AL547463 (1-925)
Qy 22 LysTrpSerGlnAlaProMetAlaGluGlyGlyGlnAsnHisHisGluValVal 41
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Db 404 CAGTGGGCTTGTCTGCT-----GGGAACGCTCTGTCAGAGGTGAAGTGTA 451
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Qy 42 LysPheMetAspValTyrGlnArgSerTyrCysHisProIleGluThrLeuValAspIle 61
   ||| ::::::::::::::::::::
Db 452 CCCTTCCAGGAAGTGTGGGCGGACGACTACTGCCGGCGCTGGAGAGGCTGGTGCACGTC 511
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Qy 62 PheGlnGluTyrProAspGluIleGluTyrIlePheLysProSerCysValProLeuMet 81
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Db 512 GTGTCCGAGTACCCAGGAGGTGGAGCAATGTTACCCCATCTGTGTCTCCCTGCTG 571
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QY 82 ArgCysGlyGlyCysCysAsnAspGluGlyLeuGluCysValProThrGluGluSerAsn 101  
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Db 572 CGCTGCACCGGCTGTGCGCGATGAGAACTGCACCTGTGCGGTGGAGACGGCCAAT 631  
QY 102 IleThrMetGlnIleMetArgIleLysProHisGlnGlyGlnHisIleGlyGluMetSer 121  
:::|||||||||:::|||||::: |||:::|  
Db 632 GTCACCATGCAGCTCCTAAAGATCCGTTCTGGGGACCGGCCCTCTACGTGGAGCTGACG 691  
QY 122 PheLeuGlnHisAsnLysCysGluCysArgProLysLysAspArgAlaArgGlnGluLys 141  
||| ||||||| ::||| ||||||| ||| :::|  
Db 692 TTCTCTCAGCACGTTTCGCTGCCAATGCCGCCCTCTCGGGGAGAAGATGAAGCCGGAAGG 751

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Job time : 2163 secs